

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:12:04 ; Search time 27 Seconds
(without alignments)
1967.098 Million cell updates/sec

Title: US-09-910-208B-1
Perfect score: 482
Sequence: 1 atgactaagctggagatca.....acatagatatccacaagag 276

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_epool_p/HADDAD-09-910208/runat_23022005_101806_14731/app_query.fasta_1.
-DB=pir_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208 @CGN 1 1 63 @runat_23022005_101806_14731 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : pir_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	371	77.0	91	2 A55406	calgranulin c - pi
2	319	66.2	92	2 JC4712	S-100 calcium-bind
3	236.5	49.1	122	1 A42628	calgranulin B - bo
4	211.5	43.9	114	1 B31848	calgranulin B [val
5	190.5	39.5	113	1 JN0686	calgranulin B - ra
6	187	38.8	95	2 S24146	S-100 protein p -
7	184	38.2	92	2 A26557	S-100 protein beta
8	181	37.6	92	2 A48015	S-100 protein beta
9	180	37.3	92	1 BCHUIB	S-100 protein beta
10	176	36.5	91	1 BCBOIA	S-100 protein beta
11	170	35.3	89	1 I56163	calgranulin A - mo
12	170	35.3	89	1 JN0685	calgranulin A - ra
13	169	35.1	95	1 S35985	S-100 protein alph
14	164.5	34.1	113	1 S68242	calgranulin B - mo

15	164	34.0	94	1 BCBOIA	S-100 protein alph
16	163	33.8	94	1 BCHUIA	S-100 protein alph
17	160	33.2	93	1 BCHUCF	calgranulin A [val
18	160	33.2	101	2 S06207	calvasculin - mous
19	157	32.6	101	2 S01759	calvasculin - rat
20	155	32.2	100	2 A53217	placental calcium-
21	155	32.2	591	2 A45135	profilaggrin - hum
22	153	31.7	101	2 A48219	calvasculin - huma
23	152.5	31.6	79	1 KLPGI	calcium-binding pr
24	148.5	30.8	79	1 JN0246	calcium-binding pr
25	146	30.3	306	2 A48118	major epidermal ca
26	145.5	30.2	79	1 KLBOI	calcium-binding pr
27	139.5	28.9	97	1 JH0663	calpactin I light
28	139.5	28.9	97	2 A28489	calpactin I light
29	136.5	28.3	95	2 A31373	calpactin I light
30	136	28.2	90	1 BCHUY	calpactin - human
31	135	28.0	90	1 S27011	calpactin - rabbit
32	135	28.0	102	1 JQ1300	calgizzarin - rabb
33	134.5	27.9	95	1 LUPG10	calpactin I light
34	134.5	27.9	97	2 JC1139	calpactin I light
35	134.5	27.9	97	2 B28489	calpactin I light
36	134.5	27.9	1130	2 T30251	repetin - mouse
37	133	27.6	1407	1 S28589	trichohyalin - rab
38	132.5	27.5	79	1 KLRTI	calcium-binding pr
39	131	27.2	89	2 A54314	calpactin - mouse
40	128	26.6	90	2 B28363	calpactin - rat
41	128	26.6	105	1 I37080	calgizzarin - huma
42	127	26.3	98	2 A41988	S-100 calcium-bind
43	127	26.3	1549	1 A40691	trichohyalin - she
44	126.5	26.2	98	2 JC5064	S-100 calcium-bind
45	126	26.1	97	2 A30129	S-100 protein, lun

ALIGNMENTS

RESULT 1
A55406

calgranulin c - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55406
R/Dell'Angelica, E.C.; Schleicher, C.H.; Santome, J.A.
J. Biol. Chem. 269, 28929-28936, 1994
A/Title: Primary structure and binding properties of calgranulin C, a novel S100-like c
A/Reference number: A55406; MUID:95050708; PMID:7961855
A/Accession: A55406
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-91
A/Cross-references: UNIPROT:P80310
C/Superfamily: S-100 protein; calmodulin repeat homology
C/Keywords: calcium binding; EF hand
F/48-80/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.: 1.14e-33 Length: 91
Score: 371.00 Matches: 74
Percent Similarity: 91.21% Conservative: 9
Best Local Similarity: 81.32% Mismatches: 8
Query Match: 76.97% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x A55406 (1-91)

QY	4	ACTAAGCTGGAAGATCACTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTCGG 63
Db	1	ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY	64	GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACCTT 123
		:::
Db	21	LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY	124	CCAAAACCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGACCTG 183

Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
QY 184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTGGTGTCCAGGGTG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValIleuValThrAspVal 80
QY 244 CTGAAAACAGCCCATAGATATCCACAAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91
RESULT 2
S-100 calcium-binding protein A12 - human
N;Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; calg
utrophil protein
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4712; JC4717; JC4891; S56113; S56114
R;Yamamura, T.; Hitomi, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsukada,
Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A;Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping.
A;Reference number: JC4712; MUID:96192053; PMID:8619860
A;Accession: JC4712
A;Molecule type: mRNA
A;Residues: 1-92 <YAM>
A;Cross-references: UNIPROT:P80511; DDBJ:D83657; NID:g1502284; PIDN:BAA12030.1; PID:g150
R;Martí, T.; Ertmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A;Title: Host-parasite interaction in human onchocerciasis: Identification and sequence
A;Reference number: JC4717; MUID:96192069; PMID:8619876
A;Accession: JC4717
A;Molecule type: protein
A;Residues: 2-92 <MAR>
A;Experimental source: Onchocerca volvulus infecting human tissue
R;Ilg, E.C.; Troxler, H.; Buergisser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hunz
Biochem. Biophys. Res. Commun. 225, 146-150, 1996
A;Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP, C
A;Reference number: JC4891; MUID:96332419; PMID:8769108
A;Accession: JC4891
A;Molecule type: protein
A;Residues: 2-92 <ILG>
R;Guignard, F.; Mauel, J.; Markert, M.
Biochem. J. 309, 395-401, 1995
A;Title: Identification and characterization of a novel human neutrophil protein related
A;Reference number: S56113; MUID:95351965; PMID:7626002
A;Accession: S56113
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'xx',4-14,'x',16-17,'xxxx' <GUI1>
A;Experimental source: isoform 6a
A;Accession: S56114
A;Status: preliminary
A;Molecule type: protein
A;Residues: 2-21 <GUI2>
A;Experimental source: isoform 6b
C;Comment: This protein is released by activated neutrophils in the course of inflammat
C;Genetics:
A;Gene: GDB:S100A12; p6; MRP6; CGRP; CAAF1
A;Cross-references: GDB:5218374
A;Map position: 1q21-1q21
C;Complex: monomer
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
F;2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAR>
F;6-39/Domain: calmodulin repeat homology <EF1>
F;49-81/Domain: calmodulin repeat homology <EF2>
F;86-90/Region: zinc binding #status predicted
Alignment Scores:
Pred. No.: 8.75e-28 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13

Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-1 (1-276) x JC4712 (1-92)
QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGTTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCCCAAAACCCTCCAGAACACCAAAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCCGATAAAGACGGAGCCGTCAGCTTTTGAGGAATTCGTAGTCTGTGTCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCACATAGATATCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 3
A42628
calgranulin B - bovine (fragment)
N;Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory facto
in 2
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997
C;Accession: B22309; A42628
R;Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,
submitted to the Protein Sequence Database, July 1992
A;Reference number: A22309
A;Accession: B22309
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-122 <TAN>
R;Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.
Biochemistry 31, 5898-5905, 1992
A;Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophil
A;Reference number: A42628; MUID:92304974; PMID:1610833
A;Accession: A42628
A;Molecule type: protein
A;Residues: 4-32,'F',34-56 <DIA>
C;Complex: heterodimer and higher complexes with calgranulin A
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phos
F;6-40/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
Alignment Scores:
Pred. No.: 2.01e-18 Length: 122
Score: 236.50 Matches: 45
Percent Similarity: 75.82% Conservative: 24
Best Local Similarity: 49.45% Mismatches: 21
Query Match: 49.07% Indels: 1
DB: 1 Gaps: 1
US-09-910-208B-1 (1-276) x A42628 (1-122)
QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetSerGlnMetGluSerSerIleGluThrIleIleAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGTTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLeuGlyHisTyrAspThrLeuIleGlnLysGluSerLysGlnLeuValGlnLysGlu 40
QY 121 CTTCCCAAAACCCTC---CAGAACACCAAAAGATCAACCTACCATTGACAAAATATTCCAA 177

Db 41 LeuSerHisPheLeuGluGluIleLysGluGlnGluValValAspLysValMetGluThr 60
QY 181 CTGGATCCGATAAAGACGAGCGTCAGCTTTGAGGAATTCGTAGTCCTCGTGTCCAGG 240
Db 61 LeuAspGluAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValSerMet 80
QY 241 GTGCTGAAACAGCCCCAC 258
Db 81 ValThrThrAlaCysHis 86
RESULT 8
A48015
S-100 protein beta chain - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C/Accession: A48015
R/Jiang, H.; Shah, S.; Hilt, D.C.
J. Biol. Chem. 268, 20502-20511, 1993
A/Title: Organization, sequence, and expression of the murine S100beta gene. Transcripti
A/Reference number: A48015; MUID:93388628; PMID:8376406
A/Accession: A48015
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-92<JIA>
A/Cross-references: UNIPROT:P50114; GB:L22144; PIDN:AAA03075.1; PID:9404769
C/Genetics:
A/Introns: 46/3
C/Superfamily: S-100 protein; calmodulin repeat homology
C/Keywords: acetylated amino end; calcium binding; EF hand
F/2-92/Product: S-100 protein beta chain #status predicted <MAT>
F/6-40/Domain: calmodulin repeat homology <EF1>
F/49-81/Domain: calmodulin repeat homology <EF2>
F/2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F/20,22,24,27,32/Binding site: calcium (Gly, Glu, Asp, Lys, Glu) #status predicted
F/62,64,66,68,70,73/Binding site: calcium (Asp, Asp, Glu, Asp, Glu) #status predict
Alignment Scores:
Pred. No.: 3.63e-12 Length: 92
Score: 181.00 Matches: 36
Percent Similarity: 59.30% Conservative: 15
Best Local Similarity: 41.86% Mismatches: 35
Query Match: 37.55% Indels: 0
DB: 2
US-09-910-208B-1 (1-276) x A48015 (1-92)
QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetSerGluLeuGluLysAlaMetValAlaLeuIleAspValPheHisGlnTyrSerGly 20
QY 61 CGGGTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgGluGlyAspLysHisLysLeuLysLysSerGluLeuLysGluLeuIleAsnAsnGlu 40
QY 121 CTTCCTCCAAACCCCTCCAGAACACCAAGATCAACCTACCATTTGACAAAATATTTCCAAGAC 180
Db 41 LeuSerHisPheLeuGluGluIleLysGluGlnGluValValAspLysValMetGluThr 60
QY 181 CTGGATCCGATAAAGACGAGCGTCAGCTTTGAGGAATTCGTAGTCCTCGTGTCCAGG 240
Db 61 LeuAspGluAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValAlaMet 80
QY 241 GTGCTGAAACAGCCCCAC 258
Db 81 ValThrThrAlaCysHis 86
RESULT 9
BCHUIB
S-100 protein beta chain [validated] - human
N/Alternate names: neural S-100 calcium-binding protein beta
C/Species: Homo sapiens (man)
C/Date: 04-Dec-1986 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: A38364; A92972; A03076
R/Allore, R.J.; Friend, W.C.; O'Hanlon, D.; Neilson, K.M.; Bauman, R.; Dunn, R.J.; Marke
J. Biol. Chem. 265, 15537-15543, 1990
A/Title: Cloning and expression of the human S100beta gene.
A/Reference number: A38364; MUID:90368757; PMID:2394738
A/Accession: A38364
A/Molecule type: DNA
A/Residues: 1-92 <ALL>
A/Cross-references: UNIPROT:P04271; GB:J05600; GB:M59486; NID:G337726; GB:M59487; NID:G3
R/Jensen, R.; Marshak, D.R.; Anderson, C.; Lukas, T.J.; Watterson, D.M.
J. Neurochem. 45, 700-705, 1985
A/Title: Characterization of human brain S100 protein fraction: amino acid sequence of
A/Reference number: A92972; MUID:85291729; PMID:4031854
A/Accession: A92972
A/Molecule type: protein
A/Residues: 2-92 <JEN>
R/Baudier, J.; Glasser, N.; Haglid, K.; Gerard, D.
Biochim. Biophys. Acta 790, 164-173, 1984
A/Title: Purification, characterization and ion binding properties of human brain S100b
A/Reference number: A90653; MUID:85023393; PMID:6487634
A/Contents: annotation; metal ion-binding properties
C/Comment: This protein binds p53, tubulin and many other proteins at physiological con
C/Comment: S-100 is an intracellular protein that binds calcium. It binds zinc more tigi
different affinities exist for both ions on each monomer. Physiological concentrations
nding sites.
C/Comment: This protein is expressed predominantly in brain tissue by astroglial cells.
C/Comment: The homodimer contains disulfide bonds, but the bond pattern has not been der
C/Genetics:
A/Gene: GDB:S100B
A/Cross-references: GDB:120360; OMIM:176990
A/Map position: 21q22.3-21q22.3
A/Introns: 46/3
A/Note: the first intron occurs before the initiator codon
C/Complex: homodimer; heterodimer with S-100 protein alpha chain (see PIR:BCHUIA)
C/Superfamily: S-100 protein; calmodulin repeat homology
C/Keywords: blocked amino end; brain; calcium binding; EF hand; heterodimer; homodimer;
F/2-92/Product: S-100 protein beta chain #status experimental <MAT>
F/6-40/Domain: calmodulin repeat homology <EF1>
F/49-81/Domain: calmodulin repeat homology <EF2>
F/2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
F/19,22,24,27,32/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
F/62,64,66,68,73/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted
Alignment Scores:
Pred. No.: 4.7e-12 Length: 92
Score: 180.00 Matches: 36
Percent Similarity: 59.30% Conservative: 15
Best Local Similarity: 41.86% Mismatches: 35
Query Match: 37.34% Indels: 0
DB: 1
US-09-910-208B-1 (1-276) x BCHUIB (1-92)
QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetSerGluLeuGluLysAlaMetValAlaLeuIleAspValPheHisGlnTyrSerGly 20
QY 61 CGGGTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgGluGlyAspLysHisLysLeuLysLysSerGluLeuLysGluLeuIleAsnAsnGlu 40
QY 121 CTTCCTCCAAACCCCTCCAGAACACCAAGATCAACCTACCATTTGAGGAATTCGTAGTCCTCGTGTCCAGG 180
Db 41 LeuSerHisPheLeuGluGluIleLysGluGlnGluValValAspLysValMetGluThr 60
QY 181 CTGGATCCGATAAAGACGAGCGTCAGCTTTGAGGAATTCGTAGTCCTCGTGTCCAGG 240
Db 61 LeuAspAsnAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValAlaMet 80
QY 241 GTGCTGAAACAGCCCCAC 258
Db 81 ValThrThrAlaCysHis 86

QY 244 CTGAACAGCCACATAGATATCCACAAGAG 276
Db 79 GlyValAlaSerHisLysAspSerHisLysGlu 89

RESULT 12

JN0685
calgranulin A - rat
N;Alternate names: calcium-binding protein MRP-8; macrophage migration inhibitory factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 23-May-1997 #text_change 09-Jul-2004
C;Accession: JN0685
R;Inamichi, T.; Uchida, I.; Wahli, S.M.; McCartney-Francis, N.
Biochem. Biophys. Res. Commun. 194, 819-825, 1993
A;Title: Expression and cloning of migration inhibitory factor-related protein (MRP) 8 an
A;Reference number: JN0685; MUID:93343942; PMID:8343166
A;Accession: JN0685
A;Molecule type: mRNA
A;Residues: 1-89 <INA>
A;Cross-references: UNIPROT:P50115; GB:L18891; NID:G349548; PIDN:AAA41637.1; PID:G349549
A;Experimental source: strains LEW/N and F344/N
C;Comment: This protein has a role in susceptibility to SCW-induced chronic disease.
C;Genetics:

A;Gene: MRP8
C;Complex: homodimer; heterodimer and higher complexes with calgranulin B
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; cytokine; EF hand; heterodimer; homodimer; inflammation
F;7-41/Domain: calmodulin repeat homology <EF1>
F;46-78/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.: 6.33e-11 Length: 89
Score: 170.00 Matches: 34
Percent Similarity: 60.44% Conservative: 21
Best Local Similarity: 37.36% Mismatches: 32
Query Match: 35.27% Indels: 4
DB: 1 Gaps: 1

US-09-910-208B-1 (1-276) x JN0685 (1-89)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGAATCATCAATCTTCCACCAGTACTCCGTTCCG 63
Db 3 ThrGluLeuGluLysAlaLeuSerAsnValIleGluValTyrHisAsnTyrSerGlyIle 22
QY 64 GTGGGCATTTTCGACACCCCTCAACAAGCGTGAGTGAAGCAGCTGATCATCAAGGAAC 123
Db 23 LysGlyAsnHisHisAlaLeuTyrArgAspAspPheArgLysMetValThrGluCys 42
QY 124 CCCAAACCTCCAGAACCAAGATCAACCTACCATTGACAAAATATTCGAAGACCTG 183
Db 43 ProGlnPheValGlnAsn-----LysAsnThrGluSerLeuPheLysGluLeu 58
QY 184 GATCGCGATAAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCTCGTGTCCAGGGTG 243
Db 59 AspValAsnSerAspAsnAlaIleAsnPheGluGluPheLeuAlaLeuValIleArgVal 78
QY 244 CTGAACAGCCACATAGATATCCACAAGAG 276
Db 79 GlyValAlaAlaHisLysAspSerHisLysGlu 89

RESULT 13

S35985
S-100 protein alpha chain - weatherfish
C;Species: Misgurnus fossilis (weatherfish)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S35985
R;Ivanenkov, V.V.; Gerke, V.; Minin, A.A.; Plessmann, U.; Weber, K.
Mech. Dev. 42, 151-158, 1993
A;Title: Transduction of Ca(2+) signals upon fertilization of eggs; identification of an
A;Reference number: S35985; MUID:94031845; PMID:8217841
A;Accession: S35985
A;Molecule type: protein
A;Residues: 1-95 <IVA>
A;Cross-references: UNIPROT:Q7LZT1

C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand
F;49-81/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.: 8.32e-11 Length: 95
Score: 169.00 Matches: 35
Percent Similarity: 64.56% Conservative: 16
Best Local Similarity: 44.30% Mismatches: 28
Query Match: 35.06% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S35985 (1-95)

QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAATCTTCCACCAGTACTCCGTT 60
Db 1 ValSerGlnLeuGluSerAlaMetGluSerLeuIleLysValPheHisThrTyrSerSer 20
QY 61 CGGTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 LysGluGlyAspLysTyrLysLeuSerLysAlaGluLeuLysSerLeuGlnGlyGlu 40
QY 121 CTTCCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTTCAAGAC 180
Db 41 LeuAsnAspPheLeuSerAlaSerLysAspProMetValValGluLysIleMetSerAsp 60
QY 181 CTGGATCCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGTGTCC 237
Db 61 LeuAspGluAsnGlnAspGlyGluValAspPheGlnGluPheValValLeuValAla 79

RESULT 14

S68242
calgranulin B - mouse
N;Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor
C;Species: Mus musculus (house mouse)
C;Date: 06-Sep-1996 #sequence_revision 23-May-1997 #text_change 09-Jul-2004
C;Accession: S68242; S68272
R;Lagasse, E.; Weissman, I.L.
submitted to the EMBL Data Library, February 1992
A;Description: Mouse MRP8 and MRP14, two intracellular calcium-binding proteins associa
A;Reference number: S68242
A;Accession: S68242
A;Molecule type: mRNA
A;Residues: 1-113 <LAG>
A;Cross-references: UNIPROT:P31725; EMBL:M83219; NID:G199807; PIDN:AAB07228.1; PID:G199
R;Raftery, M.J.; Harrison, C.A.; Alewood, P.; Jones, A.; Geczy, C.L.
Biochem. J. 316, 285-293, 1996
A;Title: Isolation of the murine S100 protein MRP14 (14 kDa migration-inhibitory-factor
ding.
A;Reference number: S68272; MUID:96235204; PMID:8645219
A;Accession: S68272
A;Molecule type: protein
A;Residues: 2-10;95-109 <RAF>
A;Note: 107-His is identified as 3'-methylhistidine; the authors' source for the refere
ylhistidine
C;Genetics:

A;Gene: MRP14
C;Complex: heterodimer and higher complexes with calgranulin A
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation; u
F;2-113/Product: calgranulin B #status predicted <MAT>
F;11-45/Domain: calmodulin repeat homology <EF1>
F;55-87/Domain: calmodulin repeat homology <EF2>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F;80-91/Disulfide bonds: #status experimental
F;103,105,107/Binding site: zinc (His) #status predicted
F;107/Modified site: 3'-methylhistidine (His) #status experimental

Alignment Scores:

Pred. No.: 2.78e-10 Length: 113
Score: 164.50 Matches: 31
Percent Similarity: 67.03% Conservative: 30
Best Local Similarity: 34.07% Mismatches: 29

Query Match:	34.13%	Indels:	1
DB:	1	Gaps:	1
US-09-910-208B-1 (1-276) x S68242 (1-113)			
QY	4	ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCACCAGTACTCCGTTCCG 63	
Db	7	SerGlnMetGluArgSerIleThrThrIleAspThrPheHisGlnTyrSerArgLys 26	
QY	64	GTGGGGCATTTTCGACACCTCAACAAGCTGAGCTGAAGCAGCTGATCACAAGAACTT 123	
Db	27	GluGlyHisProAspThrLeuSerLysLysGluPheArgGlnMetValGluAlaGlnLeu 46	
QY	124	CCCAAAACCTCCAGAACACCAAA---GATCAACCTACCATTCGACAAAATATTCCAAGAC 180	
Db	47	AlaThrPheMetLysLysGluLysArgAsnGluAlaLeuIleAsnAspIleMetGluAsp 66	
QY	181	CTGGATGCCGATAAAGACGGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTCCAGG 240	
Db	67	LeuAspThrAsnGlnAspAsnGlnLeuSerPheGluGluCysMetMetLeuMetAlaLys 86	
QY	241	GTGCTGAAAACAGCCACATAGATATCCACAA 273	
Db	87	LeuIlePheAlaCysHisGluLysLeuHisGlu 97	
RESULT 15			
BCBOIA			
S-100 protein alpha chain - bovine			
C;Species: Bos primigenius taurus (cattle)			
C;Date: 14-Nov-1983 #sequence revision 06-Feb-1995 #text_change 09-Jul-2004			
C;Accession: A24156; A91110; S54346; A03078			
R;Kuwano, R.; Maeda, T.; Usui, H.; Araki, K.; Yamakuni, T.; Ohshima, Y.; Kurihara, T.; T			
FEBS Lett. 202, 97-101, 1986			
A;Title: Molecular cloning of cDNA of S100alpha subunit mRNA.			
A;Reference number: A24156; MUID:86248083; PMID:3755105			
A;Accession: A24156			
A;Molecule type: mRNA			
A;Residues: 1-94 <KUW>			
A;Cross-references: UNIPROT:P02639			
R;Isobe, T.; Okuyama, T.			
Eur. J. Biochem. 116, 79-86, 1981			
A;Title: The amino-acid sequence of the alpha subunit in bovine brain S-100 a protein.			
A;Reference number: A91110; MUID:81236562; PMID:7250124			
A;Accession: A91110			
A;Molecule type: protein			
A;Residues: 2-64,'D',66-94 <ISO>			
R;Baudier, J.; Gerard, D.			
Biochemistry 22, 3360-3369, 1983			
A;Title: Ions binding to S100 proteins: structural changes induced by calcium and zinc c			
A;Reference number: A90471; MUID:84000339; PMID:6615778			
A;Contents: annotation; metal ion-binding properties			
R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.			
Biochem. J. 306, 551-555, 1995			
A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia			
A;Reference number: S54343; MUID:95194333; PMID:7887910			
A;Accession: S54346			
A;Molecule type: protein			
A;Residues: 24-33 <OKA>			
C;Comment: The S-100 protein is composed of two related polypeptide chains, alpha and be			
brain proteins, S-100 is also found in a variety of other tissues.			
C;Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc ve			
es, with different affinities, exist for both ions on each monomer. Physiological concen			
alcium-binding sites.			
C;Superfamily: S-100 protein; calmodulin repeat homology			
C;Keywords: blocked amino end; brain; calcium binding; EF hand; zinc			
F;2-94/Product: S-100 protein alpha chain #status predicted <MAT>			
F;7-41/Domain: calmodulin repeat homology <EF1>			
F;50-82/Domain: calmodulin repeat homology <EF2>			
F;2/Modified site: blocked amino end (Gly) (in mature form) (probably acetylated) #statu			
F;20,23,25,28,33/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted			
F;63,65,67,69,74/Binding site: calcium (Asp, Asn, Asp, Glu, Glu) #status predicted			

Alignment Scores:

Pred. No.:	3.06e-10	Length:	94
Score:	164.00	Matches:	33
Percent Similarity:	66.67%	Conservative:	19
Best Local Similarity:	42.31%	Mismatches:	26
Query Match:	34.02%	Indels:	0
DB:	1	Gaps:	0
US-09-910-208B-1 (1-276) x BCBOIA (1-94)			
QY	4	ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCACCAGTACTCCGTTCCG 63	
Db	3	SerGluLeuGluThrAlaMetGluThrLeuIleAsnValPheHisAlaHisSerGlyLys 22	
QY	64	GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123	
Db	23	GluGlyAspLysTyrLysLeuSerLysLysGluLeuLysGluLeuGlnThrGluLeu 42	
QY	124	CCCAAAACCTCCAGAACACCAACATCAACCTACCATTCGACAAAATATTCCAAGACCTG 183	
Db	43	SerGlyPheLeuAspAlaGlnLysAspAlaAspAlaValAspLysValMetLysGluLeu 62	
QY	184	GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCC 237	
Db	63	AspGluAsnGlyAspGlyGluValAspPheGlnGluTyrValValLeuValAla 80	

Search completed: February 23, 2005, 11:23:47

Job time : 28 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:11:14 ; Search time 116 Seconds
(without alignments)
2436.791 Million cell updates/sec

Title: US-09-910-208B-1
Perfect score: 482
Sequence: 1 atgactaagctggaagatca.....acatagatatccacaagag 276

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/HADDAD-09-910208/runat_23022005_101805_14722/app_query.fasta_1.
-DB=UniProt_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208 @CGN_1_1_244 @runat_23022005_101805_14722 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query		Description	
No.	Score	Match	Length DB ID		
1	465	96.5	91	1	S112_BOVIN
2	371	77.0	91	1	S112_PIG
3	349	72.4	70	2	Q9TR16
4	314	65.1	91	1	S112_HUMAN
5	274	56.8	81	1	S112_RABIT
6	238.5	49.5	122	1	S109_BOVIN
7	211.5	43.9	114	1	S109_HUMAN
8	210.5	43.7	118	1	S109_RABIT
9	210	43.6	119	2	Q6PRV2
10	202	41.9	119	1	M126_CHICK
11	195	40.5	100	2	Q7ZVA4
12	190.5	39.5	111	2	Q761U7
13	190.5	39.5	112	1	S109_RAT
14	187	38.8	95	1	S10P_HUMAN
15	185	38.4	92	2	Q925T3
16	184	38.2	101	2	O93395

17	182	37.8	99	2	Q8AYJ2	Q8ayj2 squalus aca
18	180	37.3	92	2	Q6YNR6	Q6ynr6 oryctolagus
19	179	37.1	91	1	S10B_RAT	P04631 rattus norv
20	177	36.7	92	1	S10I ICTPU	Q91061 ictalurus p
21	176	36.5	91	1	S10B_BOVIN	P02638 bos taurus
22	176	36.5	91	1	S10B_MOUSE	P50114 mus musculu
23	175	36.3	91	1	S10B_HUMAN	P04271 homo sapien
24	175	36.3	92	2	Q9PSF6	Q9psf6 ictalurus p
25	174	36.1	88	1	S108_RAT	P50115 rattus norv
26	170	35.3	88	1	S108_MOUSE	P27005 mus musculu
27	170	35.3	95	2	Q6DGT8	Q6dgt8 brachydanio
28	169	35.1	95	1	S10A_MISFO	Q71zt1 misgurnus f
29	168	34.9	2850	1	HORN_HUMAN	Q86yz3 homo sapien
30	167	34.6	93	1	S10A_RAT	P35467 rattus norv
31	164.5	34.1	112	1	S109_MOUSE	P31725 mus musculu
32	164	34.0	93	1	S10A_BOVIN	P02639 bos taurus
33	163	33.8	93	1	S10A_HUMAN	P23297 homo sapien
34	163	33.8	98	1	S10Z_HUMAN	Q8wx98 homo sapien
35	162	33.6	79	2	Q9JL08	Q9jl08 mus musculu
36	161	33.4	94	2	Q9D3M4	Q9d3m4 mus musculu
37	161	33.4	94	2	Q91V77	Q91v77 m mus muscu
38	161	33.4	148	2	Q8BLX1	Q8blx1 mus musculu
39	161	33.4	2496	1	HORN_MOUSE	Q8vhd8 mus musculu
40	160	33.2	93	1	S108_HUMAN	P05109 h calgranul
41	160	33.2	93	1	S10A_MOUSE	P56565 mus musculu
42	160	33.2	95	2	Q6XG62	Q6xg62 brachydanio
43	160	33.2	101	1	S104_MOUSE	P07091 mus musculu
44	157	32.6	101	1	S104_RAT	P05942 rattus norv
45	155	32.2	100	1	S104_BOVIN	P35466 bos taurus

ALIGNMENTS

RESULT 1
S112_BOVIN
ID S112_BOVIN STANDARD; PRT; 91 AA.
AC P79105;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC) (Calcium-binding protein in amniotic fluid 1)
DE (CAAF1) (RAGE binding protein).
GN Name=S100A12; Synonyms=CAAF1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oesophagus;
RX MEDLINE=96298783; PubMed=8718672;
RA Hitomi J., Yamaguchi K., Kikuchi Y., Kimura T., Maruyama K.,
RA Nagasaki K.;
RT "A novel calcium-binding protein in amniotic fluid, CAAF1: its
RT molecular cloning and tissue distribution.";
RL J. Cell Sci. 109:805-815(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=99325504; PubMed=10399917; DOI=10.1016/S0092-8674(00)80801-6;
RA Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C.,
RA Kambham N., Bierhaus A., Nawroth P., Neurath M.F., Slattey T.,
RA Beach D., McClary J., Nagashima M., Morser J., Stern D., Schmidt A.M.;
RT "RAGE mediates a novel proinflammatory axis: a central cell surface
RT receptor for S100/calgranulin polypeptides.";
RL Cell 97:889-901(1999).
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; D49548; BAA08496.1; --
DR EMBL; AF011757; AAB65423.1; --
DR HSSP; P80511; IGOM.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Metal-binding; Zinc.
FT INIT_MET 0 By similarity.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

Alignment Scores:
Pred. No.: 1.76e-41 Length: 91
Score: 465.00 Matches: 91
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.47% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_BOVIN (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAAACCTCCAGAACACCAAGATCAACCTTACCATTTGACAAAATATTCCAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCCGATAAAGACGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCTGGTGTCAGGCTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAAACAGCCACATAGATATCCACAAGAG 276
Db 81 LeuLysThrAlaHisIleAspIleHisLysGlu 91

RESULT 2
S112_PIG
ID S112_PIG ; STANDARD; PRT; 91 AA.
AC P80310;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC).
GN Name=S100A12;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC TISSUE=Granulocyte;
RX MEDLINE=95050708; PubMed=7961855;
RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
RT "Primary structure and binding properties of calgranulin C, a novel
RT S100-like calcium-binding protein from pig granulocytes.";
RL J. Biol. Chem. 269:28929-28936(1994).

CC -!- TISSUE SPECIFICITY: Found essentially in granulocytes with small
CC amounts found in lymphocytes.
CC -!- MISCELLANEOUS: In the absence of zinc binds one calcium ion per
CC molecule, in the presence of zinc binds two calcium ions per
CC molecule.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
DR PIR; A55406; A55406.
DR HSSP; P80511; 1E8A.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Direct protein sequencing; Metal-binding; Zinc.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 91 AA; 10614 MW; B4204461432D7FCE CRC64;

Alignment Scores:
Pred. No.: 2.78e-31 Length: 91
Score: 371.00 Matches: 74
Percent Similarity: 91.21% Conservative: 9
Best Local Similarity: 81.32% Mismatches: 8
Query Match: 76.97% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_PIG (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAGCTT 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAAACCTCCAGAACACCAAGATCAACCTTACCATTTGACAAAATATTCCAGACCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
QY 184 GATGCCGATAAAGACGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCTGGTGTCAGGCTG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80
QY 244 CTGAAAACAGCCACATAGATATCCACAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 3
Q9TR16
ID Q9TR16 PRELIMINARY; PRT; 70 AA.
AC Q9TR16;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CORNEA-associated antigen, CO-AG=CALGRANULIN C homolog.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96181454; PubMed=8603881;
RA Liu S.H., Gottsch J.D.;
RT "Amino acid sequence of an immunogenic corneal stromal protein.";
RL Invest. Ophthalmol. Vis. Sci. 37:944-948(1996).
CC -!- SIMILARITY: Belongs to the S-100 family.
DR HSSP; P80511; 1E8A.

DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
SQ SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;

Alignment Scores:
Pred. No.: 6.66e-29 Length: 70
Score: 349.00 Matches: 68
Percent Similarity: 97.14% Conservatives: 0
Best Local Similarity: 97.14% Mismatches: 2
Query Match: 72.41% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q9TR16 (1-70)

QY 4 ACTAAGCTGGAAGATCATCCCTGGAGGGAATCATCAATCTTCCACCAGTACTCCGTTCCGG 63
|||||
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 GTGGGCATTTTCGACACCCCTCAACAGCGTGAGTGAAGCAGCTGATCACAAGGAACCTT 123
|||||
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCAGAAACCTCCAGAACACCAAGATCAACCTTACCATTGACAAAATATTCGAAGACCTG 183
|||||
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCCGATAAAGACGCGGCGTGCTTTT 213
|||||
Db 61 AspAlaAspLysLysGlyAlaValValPhe 70

RESULT 4
S112 HUMAN
ID S112_HUMAN STANDARD; PRT; 91 AA.
AC P80511; P83219;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Calgranulin C (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding
protein in amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].
GN Name=S100A12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1;
RA Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;
RT "Characterization of the human S100A12 (calgranulin C, p6, CAAF1,
CGRP) gene, a new member of the S100 gene cluster on chromosome
1q21.";
RL Cell Calcium 20:459-464(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96192053; PubMed=8619860; DOI=10.1006/bbrc.1996.0600;
RA Yamamura T., Hitomi J., Nagasaki K., Suzuki M., Takahashi E.,
RA Saito S., Tsukada T., Yamaguchi K.;
RT "Human CAAF1 gene -- molecular cloning, gene structure, and chromosome
mapping.";
RL Biochem. Biophys. Res. Commun. 221:356-360(1996).
RN [3]
RP SEQUENCE.
RX MEDLINE=96192069; PubMed=8619876; DOI=10.1006/bbrc.1996.0616;
RA Marti T., Erttmann K.D., Gallin M.Y.;
RT "Host-parasite interaction in human onchocerciasis: identification and
sequence analysis of a novel human calgranulin.";
RL Biochem. Biophys. Res. Commun. 221:454-458(1996).
RN [4]
RP SEQUENCE.

RC TISSUE=Neutrophils;
RX MEDLINE=96332419; PubMed=8769108; DOI=10.1006/bbrc.1996.1144;
RA Ilg E.C., Troxler H., Buerigisser D.M., Kuster T., Markert M.,
RA Guignard F., Hunziker P., Birchler N., Heizmann C.W.;
RT "Amino acid sequence determination of human S100A12 (p6, calgranulin
C, CGRP, CAAF1) by tandem mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
RN [5]
RP SEQUENCE OF 1-20.
RX MEDLINE=95351965; PubMed=7626002;
RA Guignard F., Mael J., Markert M.;
RT "Identification and characterization of a novel human neutrophil
protein related to the S100 family.";
RL Biochem. J. 309:395-401(1995).
RN [6]
RP SEQUENCE OF 77-91, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY.
RX TISSUE=Nasal mucus;
RX MEDLINE=21413725; PubMed=11522286; DOI=10.1016/S0014-5793(01)02731-4;
RA Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;
RT "Calcitermin, a novel antimicrobial peptide isolated from human airway
secretions.";
RL FEBS Lett. 504:5-10(2001).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
RX MEDLINE=21065388; PubMed=11134923; DOI=10.1107/S090744490001458X;
RA Moroz O.V., Antson A.A., Murshudov G.N., Maitland N.J., Dodson G.G.,
RA Wilson K.S., Skibshoj I., Lukanidin E.M., Bronstein I.B.;
RT "The three-dimensional structure of human S100A12.";
RL Acta Crystallogr. D 57:20-29(2001).
CC -!- FUNCTION: Calcitermin possesses antifungal activity against
CC C.albicans and is also active against E.coli and P.aeruginosa but
CC not L.monocytogenes and S.aureus.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: Monocytes and lymphocytes.
CC -!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=1-91;
CC NOTE=Ref.6.
CC -!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=77-91;
CC NOTE=Ref.6.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.

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CC or send an email to license@isb-sib.ch).

CC EMBL; X97859; CAA66453.1; -
CC EMBL; X98288; CAA66934.1; -
CC EMBL; X98289; CAA66934.1; JOINED.
CC EMBL; X98290; CAA66934.1; JOINED.
CC EMBL; X98289; CAB94792.1; -
CC EMBL; X98290; CAB94792.1; JOINED.
CC EMBL; D49549; BAA08497.1; -
CC EMBL; D83664; BAA12036.1; -
CC EMBL; D83657; BAA12030.1; -
CC PIR; JC4712; JC4712.
CC PDB; 1E8A; X-ray; A/B=1-91.
CC PDB; 1GQM; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-91.
CC PDB; 1ODB; X-ray; A/B/C/D/E/F=1-91.
CC Genew; HGNC:10489; S100A12.
CC MIM; 603112; -
CC GO; GO:0005829; C:cytosol; TAS.
CC GO; GO:0005626; C:insoluble fraction; TAS.
CC GO; GO:0005509; F:calcium ion binding; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC InterPro; IPR001751; CaBP_S100.
CC InterPro; IPR002048; EF-hand.
CC InterPro; IPR010983; EF_Hand_like.
CC Pfam; PF00036; efhand; 1.
CC Pfam; PF01023; S_100; 1.

DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW 3D-structure; Antibiotic; Calcium-binding; Direct protein sequencing;
KW Fungicide; Metal-binding; Zinc.
FT INIT_MET 0 0
FT PEPTIDE 77 91 Calcitermin.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
FT HELIX 2 18
FT TURN 19 19
FT TURN 24 25
FT STRAND 26 27
FT TURN 29 39
FT HELIX 41 43
FT TURN 45 48
FT HELIX 50 60
FT TURN 62 63
FT STRAND 68 69
FT HELIX 70 85
SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;

Alignment Scores:
Pred. No.: 4.26e-25 Length: 91
Score: 314.00 Matches: 60
Percent Similarity: 80.22% Conservative: 13
Best Local Similarity: 65.93% Mismatches: 18
Query Match: 65.15% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_HUMAN (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCACCAGTAGTCCGGTTCGG 63
Db 1 ThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAAGGAAC TT 123
Db 21 LysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGluLeu 40
QY 124 CCCAAAACCTCCAGAACACCAAGATCAACCTTACCATTGACAAAATATTCCAGACCTG 183
Db 41 AlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60
QY 184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGCTGCCAGSGTG 243
Db 61 AspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80
QY 244 CTGAAAACAGCCCCACATAGATATCCACAAGAG 276
Db 81 LeuLysAlaAlaHisTyrHisThrHisLysGlu 91

RESULT 5
S112_RABIT
ID S112_RABIT STANDARD; PRT; 81 AA.
AC O77791;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC) (Fragment).
GN Name=S100A12;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=New Zealand white; TISSUE=Neutrophils;
RX MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
RA Yang Z., Deveer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
RA Underwood J.R., Robinson H.C.;
RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
calgranulin C when incubated with inorganic [35S]sulfate.";

RL J. Biol. Chem. 271:19802-19809(1996).
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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DR EMBL; AF091848; AAC61770.1; -.
DR HSSP; P80511; 1E8A.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Direct protein sequencing.
FT NON_TER 1 1
FT CA_BIND 8 21 EF-hand 1; low affinity (By similarity).
FT CA_BIND 51 62 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 81 AA; 9401 MW; 95E67A209180CB66 CRC64;

Alignment Scores:
Pred. No.: 9.26e-21 Length: 81
Score: 274.00 Matches: 53
Percent Similarity: 81.48% Conservative: 13
Best Local Similarity: 65.43% Mismatches: 15
Query Match: 56.85% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_RABIT (1-81)

QY 34 ATCAACATCTTCACCAGTACTCCGTTCGGTGGGGTGGGATTCGACACCCCTCAACAGCGT 93
Db 1 IleAsnIlePheHisGlnTyrSerValArgThrGlyHistyrAspThrLeuSerLysCys 20
QY 94 GAGCTGAAGCAGCTGATCACAAAGGAACCTCCCAAAACCCTCCAGAACACCAAGATCAA 153
Db 21 GluLeuLysLysLeuIleThrThrGluLeuValAsnThrIleLysAsnThrLysAspGln 40
QY 154 CCTACCATTGACAAAATATTCCAAGACCTGGATGCCGATAAAGACGGAGCCGTCAGCTTT 213
Db 41 AlaThrValAspArgIlePheArgAspLeuAspGluAspHisGlnValAspPhe 60
QY 214 GAGGAATTCGTAGTCCTGGTGTCCAGGTGCTGAAAACAGCCACATAGATATCCACAAA 273
Db 61 LysGluPheLeuSerLeuLeuAlaSerValLeuValThrAlaHisGluAsnIleHisLys 80
QY 274 GAG 276
Db 81 Glu 81

RESULT 6
S109_BOVIN
ID S109_BOVIN STANDARD; PRT; 122 AA.
AC P28783;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin B (Neutrophil cytosolic 23 kDa protein) (P23) (BEE22)
DE (Fragment).
GN Name=S100A9;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;

RT "Dynamic changes in mRNA expression of neutrophils during the course
RT of acute inflammation in rabbits.";
RL Int. Immunol. 6:149-156(1994).
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
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DR EMBL; AF091849; AAC61771.1; -.
DR EMBL; D17404; BAA04227.1; -.
DR PIR; I46861; I46861.
DR HSSP; P06702; 1IRJ.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Repeat.
FT NON_TER 1
FT CA_BIND 9 22 EF-hand 1; low affinity (Potential).
FT CA_BIND 53 64 EF-hand 2; high affinity (Potential).
FT DOMAIN 103 118 2 X 8 AA tandem repeats of G-H-G-H-G-H-S-
FT REPEAT 103 110 H.
FT REPEAT 111 118 1.
FT SEQUENCE 118 AA; 13292 MW; 7496118E21AD5C41 CRC64;

Alignment Scores:
Pred. No.: 7.4e-14 Length: 118
Score: 210.50 Matches: 41
Percent Similarity: 75.61% Conservative: 21
Best Local Similarity: 50.00% Mismatches: 19
Query Match: 43.67% Indels: 1
DB: 1 Gaps: 1

US-09-910-208B-1 (1-276) x S109_RABIT (1-118)
QY 31 ATCATCAACATCTTCCACAGTACTCCGTTCCGGTGGGCATTTCGACACCCCTCAACAAG 90
Db 1 IleIleAsnIlePheHisGlnTyrSerValArgValGlyProArgAspSerLeuSerGln 20
QY 91 CGTGAGCTGAAGCAGCTGATCACAAGGAACCTCCCAAAACCCCTC---CAGAACACCAA 147
Db 21 LysGluPheLysGlnLeuValGlnLysGluLeuHisAsnPheLeuLysLysGluAlaArg 40
QY 148 GATCAACCTACCATTGACAAAATATTCCAAGACCTGGATGCCGATAAAGACGGACCGTC 207
Db 41 AspGluLysAlaIleAsnAspIleMetGluAspLeuAspThrAsnGlnAspLysGlnLeu 60
QY 208 AGCTTTGAGGAATTCGTAGTCCTGGTGTCCAGGTGCTGAAACACAGCCACATAGATATC 267
Db 61 SerPheGluGluPheValIleLeuMetAlaArgLeuValHisAlaSerHisGluGluMet 80
QY 268 CACAAA 273
Db 81 HisLys 82
RESULT 9
Q6PRV2
ID Q6PRV2 PRELIMINARY; PRT; 119 AA.
AC Q6PRV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE MRP protein.
GN Name=MRP;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RA Hartl M., Bister K.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; AY583752; AAT01286.1; -.
DR HSSP; P04631; 1B4C.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 119 AA; 14012 MW; 00DFB09902DC5CFB CRC64;
Alignment Scores:
Pred. No.: 8.39e-14 Length: 119
Score: 210.00 Matches: 42
Percent Similarity: 71.11% Conservative: 22
Best Local Similarity: 46.67% Mismatches: 26
Query Match: 43.57% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-1 (1-276) x Q6PRV2 (1-119)
QY 1 ATGACTAAGCTGGAAGATCACCTGAGGGAATCATCAACATCTTCCACCACTACTCCGTT 60
Db 11 LeuSerGluLeuGluLysAlaMetAspThrIleIleAspValPheHisGlnTyrSerArg 30
QY 61 CGGTGGGGCATTTTCGACACCCCTCAACAAGCCTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 31 ArgGluGlyAspAsnAspThrLeuThrLysLysGluLeuLysLeuLeuIleGluLysGln 50
QY 121 CTTCCCAAAACCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 51 LeuAlaAsnTyrLeuLysHisValLysAsnGlnValSerIleAspGlnIlePheLysAsp 70
QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTGGTGTCCAGG 240
Db 71 LeuAspGlyAsnLysAspGlnGlnLeuSerPheGlyGluValMetLeuLeuIleIleArg 90
QY 241 GTGCTGAAACACAGCCACATAGATATCCAC 270
Db 91 ValIleIleAlaThrHisGluHisLeuHis 100
RESULT 10
M126_CHICK
ID M126_CHICK STANDARD; PRT; 119 AA.
AC P28318;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein MRP-126.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Bone marrow;
RX MEDLINE=92195690; PubMed=1549365;
RA Nakano T., Graf T.;

RT "Identification of genes differentially expressed in two types of v-
RT myb-transformed avian myelomonocytic cells.";
RL Oncogene 7:527-534(1992).
CC -!- TISSUE SPECIFICITY: Expressed in v-myb-transformed myelomonocytic
CC cells.
CC
CC
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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CC
CC
CC EMBL; X61200; -; NOT_ANNOTATED_CDS.
DR HSSP; P25815; 1J55.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding.
FT CA_BIND 29 42 EF-hand 1; low affinity (Potential).
FT CA_BIND 72 83 EF-hand 2; high affinity (Potential).
SQ SEQUENCE 119 AA; 14065 MW; 2D268DAF6309AD7A CRC64;

Alignment Scores:
Pred. No.: 6.19e-13 Length: 119
Score: 202.00 Matches: 41
Percent Similarity: 70.00% Conservative: 22
Best Local Similarity: 45.56% Mismatches: 27
Query Match: 41.91% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x M126_CHICK (1-119)

QY 1 ATGACTAAGCTGGAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTCCGTT 60
Db 11 LeuSerGluLeuGluysAlaileAspValileAspValPheHisGlnTyrSerArg 30
QY 61 CGGTGGGCGATTTCGACACCCCTCAACAAGCCTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 31 ArgGluGlyAspLysAspThrLeuThrArgLysGluLeuLysLeuLeuileGluLysGln 50
QY 121 CTTCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCACAGAC 180
Db 51 LeuAlaAsnTyrLeuLysHisValLysAsnGlnValSerIleAspGlnIlePheLysasp 70
QY 181 CTGGATGCCGATAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCTGCTGCCAGG 240
Db 71 LeuAspAsnAsnLysAspGlnGlnLeuSerPheGlyGluValMetLeuLeuileileArg 90
QY 241 GTGCTGAAAACAGCCACATAGATATCCAC 270
Db 91 ValThrValAlaThrHisGluHisLeuHis 100

RESULT 11

Q7ZVA4
ID Q7ZVA4 PRELIMINARY; PRT; 100 AA.
AC Q7ZVA4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 2gc:56142.
GN ORFNames=zgc:56142;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; BC045941; AAH45941.1; -.
DR HSSP; P35467; 1K2H.
DR ZFIN; ZDB-GENE-040426-1937; zgc:56142.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 100 AA; 11157 MW; DAB81814E54CB8C8 CRC64;

Alignment Scores:
Pred. No.: 3.51e-12 Length: 100
Score: 195.00 Matches: 40
Percent Similarity: 72.00% Conservative: 14
Best Local Similarity: 53.33% Mismatches: 21
Query Match: 40.46% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q7ZVA4 (1-100)

QY 10 CTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTCCGTTCCGGTGGG 69
Db 5 LeuGluArgAlaMetGluThrLeuileThrValPheHisArgTyrSerGlyAlaGluGly 24
QY 70 CATTTCGACACCTCAACAAGCCTGAGCTGAAGCAGCTGATCACAAGGAACCTCCCAA 129
Db 25 AsnSerSerThrLeuSerArgArgGluLeuLysGlnLeuMetGluLysGluLeuAlaSer 44
QY 130 ACCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCACAGACCTGGATCC 189
Db 45 PheLeuLysSerGlnLysAspProAlaAlaValAspLysIleMetLysAspLeuAspAla 64
QY 190 GATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGGTG 234
Db 65 AsnGlyAspGlyGluValAsnPheGluGluPheValSerLeuVal 79

RESULT 12

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:08:19 ; Search time 113.5 Seconds
(without alignments)
1880.984 Million cell updates/sec

Title: US-09-910-208B-1
Perfect score: 482
Sequence: 1 atgactaagctggaagatca.....acatatagatatccacaaagag 276

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USFCO.spool_p/HADDAD-09-910208/runat_23022005_101805_14715/app_query.fasta_1.
-DB=A Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208 @CGN 1 1 224 @runat_23022005_101805_14715 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq_16Dec04:
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	97.5	92	AAW03563	Aaw03563 Calcium b
2	460	95.4	90	AAAY90765	Aay90765 Bovine CA
3	460	95.4	90	AAAY90764	Aay90764 Bovine co
4	371	77.0	91	AAW01826	Aaw01826 Component
5	371	77.0	91	AAW93819	Aaw93819 Angiotrop
6	319	66.2	92	AAW03564	Aaw03564 Calcium b
7	319	66.2	92	AAW24137	Aaw24137 Human che
8	319	66.2	92	AAB45542	Aab45542 Human S10
9	319	66.2	92	AAB31911	Aab31911 Amino aci
10	319	66.2	92	AAB31907	Aab31907 Amino aci

11	319	66.2	92	4	AAB31908	Aab31908 Amino aci
12	319	66.2	92	7	ADA93649	Ada93649 Human cal
13	319	66.2	92	8	ADN04192	Adn04192 Antipsori
14	319	66.2	92	8	ADO19540	Ado19540 Human PRO
15	319	66.2	92	8	ADR14333	Adr14333 Human NF-
16	319	66.2	92	8	ADP23921	Adp23921 PRO poly
17	319	66.2	92	8	ADS74331	Ads74331 PRO poly
18	314	65.1	91	4	AAB31909	Aab31909 Amino aci
19	293	60.8	95	4	ABG27582	Abg27582 Novel hum
20	230	47.7	50	3	AAAY90763	Aay90763 Human EN-
21	211.5	43.9	114	2	AAW17062	Aaw17062 Human mul
22	211.5	43.9	114	2	AAW60178	Aaw60178 Human cal
23	211.5	43.9	114	2	AAAY48615	Aay48615 Human bre
24	211.5	43.9	114	3	AAAY87637	Aay87637 Human cal
25	211.5	43.9	114	3	AAB45539	Aab45539 Human S10
26	211.5	43.9	114	4	ABB44613	Abb44613 Human wou
27	211.5	43.9	114	4	AAB31905	Aab31905 Amino aci
28	211.5	43.9	114	6	ABB82712	Abb82712 Human MRP
29	211.5	43.9	114	7	ADB17567	Adb17567 Human mye
30	211.5	43.9	114	7	ADE57110	Ade57110 Human Pro
31	211.5	43.9	114	7	ADE34548	Ade34548 Human mig
32	211.5	43.9	114	7	ADF09358	Adf09358 Human cal
33	211.5	43.9	114	8	ADL83164	Adl83164 Human PRO
34	211.5	43.9	114	8	ADN03968	Adn03968 Antipsori
35	211.5	43.9	114	8	ADQ30562	Adq30562 Pancreas
36	211.5	43.9	114	8	ADR14329	Adr14329 Human NF-
37	211.5	43.9	114	8	ABM80144	Abm80144 Tumour-as
38	211.5	43.9	114	8	ADP23562	Adp23562 PRO poly
39	211.5	43.9	114	8	ADS74315	Ads74315 PRO poly
40	211.5	43.9	152	4	AAM39994	Aam39994 Human pol
41	201	41.7	115	4	AAB31930	Aab31930 Amino aci
42	193	40.0	46	4	ABB43183	Abb43183 Peptide #
43	193	40.0	46	4	AAM37021	Aam37021 Peptide #
44	193	40.0	46	4	ABB26281	Abb26281 protein #
45	193	40.0	46	4	AAM76914	Aam76914 Human bon

ALIGNMENTS

RESULT 1

AAW03563
ID AAW03563 standard; protein; 92 AA.

XX AC AAW03563;

XX XX
DT 01-MAY-1997 (first entry)

XX DE Calcium binding protein CAAFL1.

XX KW Calcium binding protein; bovine; amniotic fluid; S100 protein family;
KW intracellular signal transduction; squamous epithelial cell; neutrophil;
KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW squamous cell carcinoma; skin; oesophagus; CAAFL1; lung; blood disease.

XX OS Bos taurus.

XX PN EP731166-A2.

XX PD 11-SEP-1996.

XX PF 04-DEC-1995; 95EP-00119045.

XX PR 06-MAR-1995; 95JP-00045564.

XX PR 06-MAR-1995; 95JP-00070468.

XX PA (TOFU) TONEN CORP.

XX PA (HITO/) HITOMI J.

XX PI Hitomi J, Yamaguchi K, Yamamura T, Kimura T;

XX DR WPI; 1996-403989/41.

XX DR N-PSDB; AAT39345.

XX

PT New human or bovine calcium binding protein and related nucleic acid - is
PT a marker for inflammation, neoplasia, skin and blood diseases.
XX
XX
XX Claim 1; Page 21; 36pp; English.
XX
CC This sequence represents the CAAF1 calcium-binding protein isolated from
CC bovine amniotic fluid. CAAF1 belongs to the S100 protein family, which
CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion
CC concentration is one of the key factors for intracellular signal
CC transduction. The calcium signals are transduced by various calcium-
CC binding proteins, such as the protein encoded by this sequence. CAAF1 is
CC normally expressed in squamous epithelial cells, neutrophils and
CC macrophages, but atypical epithelial cells are negative for CAAF1 and
CC overexpression is observed in several types of cancer cells and
CC neutrophils/macrophages infiltrating cancerous lesions. Detection of
CC CAAF1 (using antibodies in usual immunoassays) can be used to diagnose
CC (or monitor) inflammation, neoplasia (particularly squamous cell
CC carcinoma of the skin, oesophagus, lung and cervix), and skin and blood
CC diseases
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 2,99e-49 Length: 92
Score: 470.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.51% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAW03563 (1-92)

QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGGTGGGGCATTTCCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGlu 40

QY 121 CTTCCAAAACCCCTCAGAACACCCAAAGATCAACCTACCATTGACAAAAATATCCAGAC 180
Db 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 60

QY 181 CTGGATCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGTCCAGG 240
Db 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg 80

QY 241 GTGCTGAAACAGCCCATAGATATCCACAAGAG 276
Db 81 ValLeuLysThrAlaHisIleAspIleHisLysGlu 92

RESULT 2
AAAY90765
ID AAY90765 standard; protein; 90 AA.
XX
AC AAY90765;
XX
DT 18-AUG-2000 (first entry)
XX
DE Bovine CAAF1 acid sequence SEQ ID NO:4.
XX
KW Bovine; EN-RAGE; extracellular novel RAGE binding protein;
KW receptor for advanced glycation endproduct; inflammation; inhibition;
KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;
KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;
KW autoimmune disorder; inflammatory disorder.
XX
OS Bos taurus.
XX
PN WO200020621-A1.
XX
PD 13-APR-2000.

XX 06-OCT-1999; 99WO-US023303.
PF
XX
PR 06-OCT-1998; 98US-00167705.
PR 05-MAR-1999; 99US-00263312.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Schmidt AM, Stern D;
XX
DR WPI; 2000-303794/26.
XX
PT New human EN-RAGE (extracellular novel receptor for advanced glycation
PT end products) peptide, useful for identifying anti-inflammatory compounds
PT that inhibit its interaction with RAGE.
XX
PS Claim 2; Page 41; 132pp; English.
XX
CC The present invention describes an isolated human EN-RAGE (extracellular
CC novel receptor for advanced glycation end products) peptide (pi). The EN-
CC RAGE peptide binds to RAGE which is a member of the immunoglobulin
CC superfamily of cell-surface molecules. A compound capable of inhibiting
CC the interaction of EN-RAGE with RAGE is useful for the suppression of
CC inflammation resulting from systemic lupus erythematosus, inflammatory
CC lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
CC inflammatory disorder in which the recruitment of EN-RAGE containing
CC inflammatory cells occurs. The compound is also useful for the treatment
CC of systemic lupus erythematosus, inflammatory lupus nephritis in a
CC subject. The human EN-RAGE peptide is useful for identifying compounds
CC that inhibit its interaction with RAGE. The present sequence represents
CC the bovine CAAF1 which shows homology to the human EN-RAGE N-terminal
CC amino acid sequence
XX
SQ Sequence 90 AA;

Alignment Scores:
Pred. No.: 5.2e-48 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x AAY90765 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 GTGGGGCATTTCCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAAATATCCAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGTCCAGGTTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAAAACAGCCCATAGATATCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 3
AAAY90764
ID AAY90764 standard; protein; 90 AA.
XX
AC AAY90764;
XX
DT 18-AUG-2000 (first entry)
XX

DE Bovine corneal antigen (B-COAg) acid sequence SEQ ID NO:3.

XX

KW Bovine; EN-RAGE; extracellular novel RAGE binding protein;

KW receptor for advanced glycation endproduct; inflammation; inhibition;

KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;

KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;

KW autoimmune disorder; inflammatory disorder.

XX

OS Bos taurus.

XX

PN WO200020621-A1.

XX

PD 13-APR-2000.

XX

PF 06-OCT-1999; 99WO-US023303.

XX

PR 06-OCT-1998; 98US-00167705.

PR 05-MAR-1999; 99US-00263312.

XX

PA (UYCO) UNIV COLUMBIA NEW YORK.

XX

PI Schmidt AM, ; Stern D;

XX

DR WPI; 2000-303794/26.

XX

PT New human EN-RAGE (extracellular novel receptor for advanced glycation end products) peptide, useful for identifying anti-inflammatory compounds that inhibit its interaction with RAGE.

PT

XX

PS Claim 2; Page 41; 132pp; English.

XX

CC The present invention describes an isolated human EN-RAGE (extracellular novel receptor for advanced glycation end products) peptide (P1). The EN-RAGE peptide binds to RAGE which is a member of the immunoglobulin superfamily of cell-surface molecules. A compound capable of inhibiting the interaction of EN-RAGE with RAGE is useful for the suppression of inflammation resulting from systemic lupus erythematosus, inflammatory lupus nephritis, septic shock, endotoxaemia, or an autoimmune or inflammatory disorder in which the recruitment of EN-RAGE containing inflammatory cells occurs. The compound is also useful for the treatment of systemic lupus erythematosus, inflammatory lupus nephritis in a subject. The human EN-RAGE peptide is useful for identifying compounds that inhibit its interaction with RAGE. The present sequence represents the bovine corneal antigen which shows homology to the human EN-RAGE N-terminal amino acid sequence

XX

SQ Sequence 90 AA;

Alignment Scores:

Pred. No.:	5.2e-48	Length:	90
Score:	460.00	Matches:	90
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.44%	Indels:	0
DB:	3	Gaps:	0

US-09-910-208B-1 (1-276) x AAY90764 (1-90)

QY 4 ACTAAGCTGGAAGATCACCCTGAGGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63

Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123

Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCCAAAACCTCCAGAACCAAGATCAACCTACCATTGACAAATATTCCAAGACCTG 183

Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATCCCGATAAAGACGGAGCCGTTCAGCTTTTGAGGAATTCGTAGTCCCTGGTGTCCAGGG 243

Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAAACAGCCCATAGATATCCACAA 273

Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 4

AAW01826

XX AAW01826 standard; protein; 91 AA.

XX

AC AAW01826;

XX

DT 16-OCT-1997 (first entry)

XX

DE Component of bioactive metal RNA polypeptide.

XX

KW Bioactive; metal; RNA polypeptide; RNP; modulation; analysis;

KW angiogenesis; vascular state; mammalian tissue; transfer; cell;

KW genetic information; selective; alteration; nucleic acid content;

KW leukocyte; pig; monocyto-CuRNP.

XX

OS Sus scrofa.

XX

PN DE19628895-A1.

XX

PD 23-JAN-1997.

XX

PF 17-JUL-1996; 96DE-01028895.

XX

PR 17-JUL-1995; 95DE-01025992.

PR 18-AUG-1995; 95DE-01030500.

XX

PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX

PI Wissler JH, Logemann E, Kieseewetter S, Heilmeyer LMG;

XX

DR WPI; 1997-088586/09.

DR N-PSDB; AAT62569.

XX

PT Bioactive metal RNA polypeptide - useful for modulating angiogenesis, etc.

PT

XX

PS Claim 1; Page 15; 16pp; German.

XX

CC A novel bioactive metal RNA polypeptide (RNP) has a RNA component including the sequence AAT62568 and a polypeptide component having the sequence AAW01826, which is encoded by AAT62569. The RNP, or anti-RNP immunoglobulins, can be used to modulate and/or analyse angiogenesis and the vascular state of mammalian tissue, transfer genetic information in cells and selectively alter the nucleic acid content of cells. Leukocytes from pig's blood were cultured in medium, and the supernatant treated with NH4 sulphate at 35, 45 and 90% saturation to precipitate protein fractions. The residual supernatant was diltued to 45% NH4 sulphate saturation and concentrated by ultrafiltration using a 0.5 kD membrane. The retenate was purified to give 8 mg of product described as monocyto-CuRNP

XX

SQ Sequence 91 AA;

Alignment Scores:

Pred. No.:	6.12e-37	Length:	91
Score:	371.00	Matches:	74
Percent Similarity:	91.21%	Conservative:	9
Best Local Similarity:	81.32%	Mismatches:	8
Query Match:	76.97%	Indels:	0
DB:	2	Gaps:	0

US-09-910-208B-1 (1-276) x AAW01826 (1-91)

QY 4 ACTAAGCTGGAAGATCACCCTGAGGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63

Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123

Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACCTACCTTGACAAATATTTCCAAGACCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
QY 184 GATGCCGATAAAGACGGAGCCGTGAGCTTTGAGGAATTCGTAGTCCTGCTCCAGGGTG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80
QY 244 CTGAAAACAGCCCATAGATATCCACAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91
RESULT 5
AAW93819
ID AAW93819 standard; peptide; 91 AA.
XX
AC AAW93819;
XX
DT 21-JUN-1999 (first entry)
XX
DE Angiotropin related protein derived peptide.
XX
KW Angiotropin related protein; ARP; ternary complex; S100 protein;
KW copper-containing ribonucleoprotein; copper; cell selective;
KW morphogenic action; blood capillary endothelial cell; confluent;
KW non-mitogenic induction; cell phenotype; three-dimensional organoid;
KW spatiotemporal supracellular organisation; chemotropic; blood vessel;
KW tissue neovascularisation; angiogenesis modulation.
XX
OS Synthetic.
XX
PN DE19811047-C1.
XX
PD 15-APR-1999.
XX
PF 13-MAR-1998; 98DE-01011047.
XX
PR 13-MAR-1998; 98DE-01011047.
XX
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI Kieseewetter S, Kuhn E, Koch-Pelster B, Brunner H;
XX
DR WPI; 1999-216114/19.
XX
PT Copper-containing ribonucleoproteins - useful for modulating
PT angiogenesis.
XX
PS Disclosure; Page 2; 16pp; German.
XX
CC This invention describes novel copper-containing ribonucleoproteins which
CC are ternary complexes of an S100 protein, copper ions, and RNA comprising
CC the following consensus sequence or its complement GGAAGAAUNNNUNUAUGN1-
CC 6CUNNUUNNNNNAAGN0-1UANAACAUN0-5CUUNAGN0- 13AGAA-AUN0-16UUAGCAG where
CC N = G, A, U or C. The ribonucleoproteins are stated to have the following
CC properties (1) cell-selective morphogenic action in vitro on isolated
CC primary and/or cloned blood capillary endothelial cells in culture for
CC the non-mitogenic induction of the change in cell phenotype from the
CC confluent state, for non-mitogenic alteration of the spatiotemporal
CC supracellular organisation of cells into three-dimensional organoid,
CC capillary-like structures in culture, (2) a specific chemotropic action
CC on blood vessels in vivo, (3) induction of directional growth of blood
CC vessels in vivo and (4) induction of neovascularisation of tissues
CC through directed ingrowth of blood vessels. Their use for modulating
CC angiogenesis is claimed
XX
SQ Sequence 91 AA;

Alignment Scores:
Pred. No.: 6.12e-37 Length: 91

Score: 371.00 Matches: 74
Percent Similarity: 91.21% Conservative: 9
Best Local Similarity: 81.32% Mismatches: 8
Query Match: 76.97% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-1 (1-276) x AAW93819 (1-91)
QY 4 ACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTGACACACCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAAGGAACCTT 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAAAACCTCCAGAACACCAAGATCAACCTACCATTGACAAAAATATTTCCAAGACCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
QY 184 GATCCCGATAAAGACGGAGCCGTGAGCTTTGAGGAATTCGTAGTCCTGCTCCAGGGTG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80
QY 244 CTGAAAACAGCCCATAGATATCCACAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91
RESULT 6
ID AAW03564 standard; protein; 92 AA.
XX
AC AAW03564;
XX
DT 01-MAY-1997 (first entry)
XX
DE Calcium binding protein CAAF1.
XX
KW Calcium binding protein; human; amniotic fluid; S100 protein family;
KW intracellular signal transduction; squamous epithelial cell; neutrophil;
KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW squamous cell carcinoma; skin; oesophagus; CAAF1; lung; blood disease.
XX
OS Homo sapiens.
XX
PN EP731166-A2.
XX
PD 11-SEP-1996.
XX
PF 04-DEC-1995; 95EP-00119045.
XX
PR 06-MAR-1995; 95JP-00045564.
PR 06-MAR-1995; 95JP-00070468.
XX
PA (TOFU) TONEN CORP.
PA (HITO/) HITOMI J.
XX
PI Hitomi J, Yamaguchi K, Yamamura T, Kimura T;
XX
DR WPI; 1996-403989/41.
DR N-PSDB; AAT39346.
XX
PT New human or bovine calcium binding protein and related nucleic acid - is
PT a marker for inflammation, neoplasia, skin and blood diseases.
XX
PS Claim 1; Page 24; 36pp; English.
XX
CC This sequence represents the CAAF1 calcium-binding protein isolated from
CC human amniotic fluid. CAAF1 belongs to the S100 protein family, which
CC includes calcyclin, MRP8, and MRP14. Intracellular calcium ion
CC concentration is one of the key factors for intracellular signal
CC transduction. The calcium signals are transduced by various calcium-
CC binding proteins, such as this protein. CAAF1 is normally expressed in

CC squamous epithelial cells, neutrophils and macrophages, but atypical
CC epithelial cells are negative for CAAf1 and overexpression is observed in
CC several types of cancer cells and neutrophils/macrophages infiltrating
CC cancerous lesions. Detection of CAAf1 (using antibodies in usual
CC immunoassays) can be used to diagnose (or monitor) inflammation,
CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,
CC lung and cervix), and skin and blood diseases
XX
SQ Sequence 92 AA;

Alignment Scores: 1.8e-30 Length: 92
Pred. No.: 319.00 Matches: 61
Score: 80.43% Conservative: 13
Percent Similarity: 66.30% Mismatches: 18
Best Local Similarity: 66.30% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-09-910-208B-1 (1-276) x AAW03564 (1-92)

Qy 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTACTCCGTT 60
1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
Qy 61 CGGTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
Qy 121 CTTCCTCCAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
Qy 181 CTGGATCCCGATAAAGACGAGCCGTCAGCTTTGAGGAATTCGTAGTCTGTGTCCAGG 240
61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
Qy 241 GTGCTGAAAACAGCCCATAGATATCCACAAAGAG 276
81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 7
AAW24137
ID AAW24137 standard; protein; 92 AA.
XX
AC AAW24137;
XX
DT 28-JAN-1998 (first entry)
XX
DE Human chemotactic cytokine I.
XX
KW chemotactic cytokine; tumour; autoimmune disease; antagonist; agonist.
XX
OS Homo sapiens.
XX
PN WO9723640-A1.
XX
PD 03-JUL-1997.
XX
PF 26-DEC-1995; 95WO-US016871.
XX
PR 26-DEC-1995; 95WO-US016871.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Alfonso P, Gentz R, Su JY;
XX
DR WPI; 1997-351075/32.
DR N-PSDB; AAT85774.
XX
PT DNA encoding chemotactic cytokine I - used to treat, e.g. tumours,
PT chronic infection, leukaemia, etc.
XX
PS Claim 12; Page 48-49; 64pp; English.

XX This is a human chemotactic cytokine I polypeptide. The encoding
CC polynucleotide, along with a vector and a host cell can be used for the
CC recombinant production of the chemotactic cytokine. Cytokine agonists and
CC antagonists can be used for the treatment of a patient requiring a
CC chemotactic cytokine I and for the treatment of a patient requiring the
CC inhibition of a chemotactic cytokine I polypeptide, respectively. The
CC chemotactic cytokine is used to treat tumours, chronic infection,
CC leukaemia and T-cell mediated autoimmune diseases
XX

Alignment Scores: 1.8e-30 Length: 92
Pred. No.: 319.00 Matches: 61
Score: 80.43% Conservative: 13
Percent Similarity: 66.30% Mismatches: 18
Best Local Similarity: 66.30% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-09-910-208B-1 (1-276) x AAW24137 (1-92)

Qy 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTACTCCGTT 60
1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
Qy 61 CGGTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
Qy 121 CTTCCTCCAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
Qy 181 CTGGATCCCGATAAAGACGAGCCGTCAGCTTTGAGGAATTCGTAGTCTGTGTCCAGG 240
61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
Qy 241 GTGCTGAAAACAGCCCATAGATATCCACAAAGAG 276
81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 8
AAB45542
ID AAB45542 standard; protein; 92 AA.
XX
AC AAB45542;
XX
DT 22-FEB-2001 (first entry)
XX
DE Human S100A12 protein.
XX
KW S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
KW calcium-binding protein; calcium homeostasis; cardiac muscle;
KW pumping capacity; myocardial cell; systolic calcium ion release;
KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
KW valve defect.
XX
OS Homo sapiens.
XX
PN DE19915485-A1.
XX
PD 19-OCT-2000.
XX
PF 07-APR-1999; 99DE-01015485.
XX
PR 07-APR-1999; 99DE-01015485.
XX
PA (KATU/) KATUS H A.
PA (REMP/) REMPPIS A.
XX
PI Katus HA, Remppis A;
XX

DR WPI; 2000-673510/66.
DR N-PSDB; AAC81812.
XX
PT Composition containing S100 protein, corresponding nucleic acid or
PT vector, useful for treating cardiomyopathy and cardiac insufficiency.
XX
PS Claim 35; Page 20; 36pp; German.
XX
CC This invention describes a novel composition for treating primary or
CC secondary cardiomyopathy or cardiac insufficiency contains at least one
CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
CC fragments, or a gene transfer vector containing (II), optionally
CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
CC proteins involved in calcium homeostasis, so their overexpression in
CC cardiac muscle will improve pumping capacity (and overall capacity) of
CC the heart. In cultured myocardial cells they increase the contraction and
CC relaxation rates associated with increased systolic calcium ion release
CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
CC used to treat cardiomyopathy (CMP) where inherited or caused by
CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
CC by pulmonary and/or arterial hypertension, and structural disease caused
CC by rhythm disorders or valve defects, generally any condition associated
CC with reduced contractile force. Unlike calmodulin, which is expressed
CC ubiquitously, (I) show tissue-specific expression and treat the
CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
CC disease
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.8e-30 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x AAB45542 (1-92)

QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGGTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
QY 121 CTTCCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCCTAGTCTCGTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCCATAGATATCCACAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 9

AAB31911
ID AAB31911 standard; protein; 92 AA.

XX AAB31911;

AC 15-MAY-2001 (first entry)

XX Amino acid sequence of a human protein.

XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;

KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
XX Homo sapiens.
OS WO200105422-A2.
PN 25-JAN-2001.
PD 17-JUL-2000; 2000WO-FR002057.
XX 15-JUL-1999; 99FR-00009372.
PR (INMR) BIOMERIEUX STELHYS.
PA Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
PI WPI; 2001-159475/16.
XX Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand.
XX Claim 1; Page 168; 209pp; French.

CC The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells

SQ Sequence 92 AA;

Alignment Scores:

Pred. No.: 1.8e-30 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x AAB31911 (1-92)

QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGGTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
QY 121 CTTCCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCCTAGTCTCGTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCCATAGATATCCACAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10	
ID	AAB31907
XX	AAB31907 standard; protein; 92 AA.
AC	AAB31907;
XX	
DT	15-MAY-2001 (first entry)
DE	Amino acid sequence of a human protein.
XX	
KW	Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW	ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW	neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW	Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW	rheumatoid polyarthritits; lupus erythematosus; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200105422-A2.
XX	
PD	25-JAN-2001.
XX	
PF	17-JUL-2000; 2000WO-FR002057.
XX	
PR	15-JUL-1999; 99FR-00009372.
XX	
PA	(INMR) BIOMERIEUX STELHYS.
XX	
PI	Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX	
DR	WPI; 2001-159475/16.
XX	
PT	Detecting, preventing and treating degenerative, neurological and
PT	autoimmune diseases, particularly multiple sclerosis, using specified
PT	polypeptides or related nucleic acid or ligand.
XX	
PS	Claim 1; Page 166-167; 209pp; French.
XX	
CC	The present sequence represents a human protein, which is used in the
CC	method of the invention. The specification describes a method which uses
CC	at least one polypeptide or polynucleotide sequence belonging to the
CC	perlecan, precursor of the retinol-binding plasma protein, precursor of
CC	the ganglioside GM2 activator, calgranulin B or saposin B protein
CC	families. The method is used for detecting, preventing or treating a
CC	degenerative, neurological and/or auto-immune disease. The
CC	polynucleotides and polypeptides are used for diagnosis, prognosis,
CC	prevention and treatment of multiple sclerosis (in its various forms and
CC	phases). They may also be useful in cases of e.g. Alzheimer's and
CC	Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC	polyarthritits and lupus erythematosus, including use as vaccines and in
CC	gene therapy (expression of sense or antisense sequences). They can also
CC	be used to assess efficacy of potential therapeutic agents, particularly
CC	compounds that reduce or inhibit toxicity towards glial cells
XX	
SQ	Sequence 92 AA;
Alignment Scores:	
Pred. No.:	1.8e-30 Length: 92
Score:	319.00 Matches: 61
Percent Similarity:	80.43% Conservative: 13
Best Local Similarity:	66.30% Mismatches: 18
Query Match:	66.18% Indels: 0
DB:	4 Gaps: 0
US-09-910-208B-1 (1-276) x AAB31907 (1-92)	
QY	1 ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACCACTACTCCGTT 60
DB	1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY	61 CGGTGGGGCATTTCGACACCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
DB	21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY	121 CTTCCAAAACCCCTCCAGAAACACCAAGATCAACCTACCATTCAGAAAAATATTCCAAGAC 180
DB	41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY	181 CTGGATCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTGCTAGTCCTGGTGTCCAGG 240
DB	61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY	241 GTGCTGAAAACAGCCACATAGATATCCACAAGAG 276
DB	81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 11	
AAB31908	
ID	AAB31908 standard; protein; 92 AA.
XX	
AC	AAB31908;
XX	
DT	15-MAY-2001 (first entry)
XX	
DE	Amino acid sequence of a human protein.
XX	
KW	Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW	ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW	neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW	Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW	rheumatoid polyarthritits; lupus erythematosus; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200105422-A2.
XX	
PD	25-JAN-2001.
XX	
PF	17-JUL-2000; 2000WO-FR002057.
XX	
PR	15-JUL-1999; 99FR-00009372.
XX	
PA	(INMR) BIOMERIEUX STELHYS.
XX	
PI	Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX	
DR	WPI; 2001-159475/16.
XX	
PT	Detecting, preventing and treating degenerative, neurological and
PT	autoimmune diseases, particularly multiple sclerosis, using specified
PT	polypeptides or related nucleic acid or ligand.
XX	
PS	Claim 1; Page 166-167; 209pp; French.
XX	
CC	The present sequence represents a human protein, which is used in the
CC	method of the invention. The specification describes a method which uses
CC	at least one polypeptide or polynucleotide sequence belonging to the
CC	perlecan, precursor of the retinol-binding plasma protein, precursor of
CC	the ganglioside GM2 activator, calgranulin B or saposin B protein
CC	families. The method is used for detecting, preventing or treating a
CC	degenerative, neurological and/or auto-immune disease. The
CC	polynucleotides and polypeptides are used for diagnosis, prognosis,
CC	prevention and treatment of multiple sclerosis (in its various forms and
CC	phases). They may also be useful in cases of e.g. Alzheimer's and
CC	Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC	polyarthritits and lupus erythematosus, including use as vaccines and in
CC	gene therapy (expression of sense or antisense sequences). They can also
CC	be used to assess efficacy of potential therapeutic agents, particularly
CC	compounds that reduce or inhibit toxicity towards glial cells
XX	
SQ	Sequence 92 AA;
Alignment Scores:	
Pred. No.:	1.8e-30 Length: 92
Score:	319.00 Matches: 61
Percent Similarity:	80.43% Conservative: 13
Best Local Similarity:	66.30% Mismatches: 18
Query Match:	66.18% Indels: 0
DB:	4 Gaps: 0
US-09-910-208B-1 (1-276) x AAB31907 (1-92)	
QY	1 ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACCACTACTCCGTT 60
DB	1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY	61 CGGTGGGGCATTTCGACACCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
DB	21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x AAB31908 (1-92)

QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGGTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCCTCCAAAACCCCTCCAGAACACCAACCAAGATCAACCTACCATTCACAAAATATTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GTGCTGAAAACAGCCACATAGATATCCACAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 12
ADA93649

ID ADA93649 standard; protein; 92 AA.
AC ADA93649;
XX
XX
DT 20-NOV-2003 (first entry)
XX
DE Human calgranulin C protein SEQ ID NO:2.
XX
XX inflammatory disease; calgranulin C; antiinflammatory; gene therapy;
KW vasculitis; Kawasaki disease; cystic fibrosis;
KW chronic inflammatory disease; ulcerative colitis; Crohn's disease;
KW chronic bronchitis; inflammatory arthritis; psoriatic arthritis;
KW rheumatoid arthritis; seronegative arthritis;
KW systemic onset juvenile rheumatoid arthritis; SOJRA; Still's disease;
KW acute inflammation; human.
XX
XX Homo sapiens.
OS
XX WO2003069341-A2.
PN
XX
XX 21-AUG-2003.
PD
XX
PF 17-FEB-2003; 2003WO-EP001575.
XX
PR 15-FEB-2002; 2002US-00077600.
XX
PA (SWIT-) SWITCH BIOTECH AG.
PA (SORG/) SORG C.
PA (ROTH/) ROTH J.
XX
PI Sorg C, Roth J;
XX
XX WPI; 2003-671681/63.
DR N-PSDB; ADA93648.
XX
XX Diagnosing, treating or preventing inflammatory diseases comprises
PT determining the amount and/or concentration of CALGRANULIN C polypeptide
PT and/or nucleic acids encoding the polypeptide present in a biological
PT sample.
XX
XX Claim 7; Page 64; 64pp; English.
PS
XX
CC The present invention describes a method for diagnosing inflammatory
CC diseases, which comprises determining the amount and/or concentration of
CC calgranulin C polypeptide and/or nucleic acids encoding the polypeptide

CC present in the biological sample. Also described are methods for treating
CC or preventing an inflammatory disease in a mammal, and medical treatment
CC of the mammal, where the treatment is based on the stage of the disease
CC to be treated or prevented. Calgranulin C has antiinflammatory activity
CC and can be used in gene therapy. The method is useful for diagnosing,
CC treating or preventing inflammatory diseases, e.g. vasculitis
CC (particularly Kawasaki disease), cystic fibrosis, chronic inflammatory
CC diseases like ulcerative colitis or Crohn's disease, chronic bronchitis,
CC inflammatory arthritis (e.g. psoriatic arthritis, rheumatoid arthritis or
CC seronegative arthritis), systemic onset juvenile rheumatoid arthritis
CC (SOJRA or Still's disease), acute inflammation above the background of a
CC chronic inflammation, an acquired infection on the background of an
CC inflammatory disease, or an exacerbation of an already present disease.
CC The method is also useful for diagnosing specific stages of inflammatory
CC diseases, for determining the risk of relapse, and for discriminating
CC between diseases with similar symptoms. The present sequence represents
CC human calgranulin C, which is used in the exemplification of the present
CC invention.

XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.8e-30 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 7 Gaps: 0

US-09-910-208B-1 (1-276) x ADA93649 (1-92)

QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGGTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCCTCCAAAACCCCTCCAGAACACCAACCAAGATCAACCTACCATTCACAAAATATTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GTGCTGAAAACAGCCACATAGATATCCACAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 13
ADN04192

ID ADN04192 standard; protein; 92 AA.
XX
AC ADN04192;
XX
XX 01-JUL-2004 (first entry)
DT
XX
DE Antipsoriatic protein sequence #291.
XX
XX antipsoriatic; gene therapy; psoriasis; diagnosis.
OS Homo sapiens.
XX
XX WO2004028479-A2.
PN
XX
XX 08-APR-2004.
PD
XX
XX 25-SEP-2003; 2003WO-US030907.
PF
XX
XX 25-SEP-2002; 2002US-0414006P.
PR
XX

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PA (GETH ) GENENTECH INC.
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-305105/28.
DR N-PSDB; ADN04191.
XX
PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
PS Claim 9; SEQ ID NO 586; 3069pp; English.
XX
CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.8e-30 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 8 Gaps: 0

US-09-910-208B-1 (1-276) x ADN04192 (1-92)
QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTACTCCGTT 60
Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGTTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCCTCCAAAACCTCCAGAACACCAAGATCAACCTACCATTTGACAAAATATTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCCGATAAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCTCGTGTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCCCACATAGATATCCACAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 14
AD019540
ID ADO19540 standard; protein; 92 AA.
XX
AC ADO19540;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polypeptide #235.
XX
KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX

PA WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
DR WPI; 2004-420067/39.
DR N-PSDB; ADO19539.
XX
PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthropathy.
XX
PS Claim 7; SEQ ID NO 470; 1731pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating polyneuropathy,
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.8e-30 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 8 Gaps: 0

US-09-910-208B-1 (1-276) x ADO19540 (1-92)
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Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGTTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCCTCCAAAACCTCCAGAACACCAAGATCAACCTACCATTTGACAAAATATTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCCGATAAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCTCGTGTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCCCACATAGATATCCACAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 15
ADR14333
ID ADR14333 standard; protein; 92 AA.
XX
AC ADR14333;
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XX 21-OCT-2004 (first entry)

DE Human NF-kappaB pathway-associated protein SeqID334.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;

KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;

KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;

KW immunosuppressive; vulnery; gene therapy; immune disorder;

KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;

KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;

KW hyper-igm syndrome; hypohidrotic ectodermal dysplasia;

KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;

KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;

KW viral replication; host cell survival; evasion of immune response;

KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;

KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;

KW autoimmune disorder; hyper immune activity;

KW aberrant acute phase response; hypercongenital condition; birth defect;

KW necrotic lesion; wound; organ transplant rejection;

KW aberrant signal transduction; proliferating disorder; cancer;

KW HIV propagation; human.

XX Homo sapiens.

OS

XX WO2004065577-A2.

PN

XX 05-AUG-2004.

PD

XX 13-JAN-2004; 2004WO-US000798.

PF

XX 14-JAN-2003; 2003US-0440068P.

PR

PR 12-MAY-2003; 2003US-0469757P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Nadler SG, Neubauer MG, Feder JN, Carman J;

XX

DR WPI; 2004-562168/54.

DR N-PSDB; ADR14332.

XX

PT New isolated polynucleotides and polypeptides associated with NF-kappaB

PT pathway, useful for diagnosing, treating, or preventing disorders or

PT diseases associated with NF-kappaB pathway.

XX

PS Claim 6; SEQ ID NO 334; 237pp; English.

XX

CC This invention relates to the novel association of protein sequences (and

CC the genes which encode them) to the NF-kappaB pathway. The invention may

CC be useful for the production of compounds with an antiinflammatory,

CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,

CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,

CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or

CC vulnery activity or for gene therapy. The proteins and nucleotides are

CC useful for diagnosing, preventing, treating, or ameliorating conditions

CC or diseases associated with the NF-kappaB pathway. The condition is an

CC immune disorder, an inflammatory disorder, an inflammatory disorder

CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,

CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-igm

CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic

CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,

CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell

CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory

CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick

CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper

CC immune activity, disorders related to aberrant acute phase responses,

CC hypercongenital conditions, birth defects, necrotic lesions, wounds,

CC organ transplant rejection, conditions related to organ transplant

CC rejection, disorders related to aberrant signal transduction,

CC proliferating disorders, cancers and HIV propagation in cells infected

CC with other viruses. The present sequence is that of a human protein which

CC is subject to the novel association with the NF-kappaB pathway of the

CC invention. Note: This sequence does not appear in the specification but

CC was obtained by the indexer from Genbank.

XX Sequence 92 AA;

SQ

Alignment Scores:

Pred. No.:	1.8e-30	Length:	92
Score:	319.00	Matches:	61
Percent Similarity:	80.43%	Conservative:	13
Best Local Similarity:	66.30%	Mismatches:	18
Query Match:	66.18%	Indels:	0
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Db	21	ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu	40
QY	121	CTTCCCAAAACCCTCCAGAACACCAAGATCAACCTACCATTTGACAAAATATTCACAGAC	180
Db	41	LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly	60
QY	181	CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCCTAGTCCTGGTGCCAGG	240
Db	61	LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle	80
QY	241	GTGCTGAAAACAGCCACATAGATATCCACAAGAG	276
Db	81	AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu	92

Search completed: February 23, 2005, 11:18:50

Job time : 116.5 secs

GenCore version 5.1.6
: Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:19:00 ; Search time 89 Seconds
(without alignments)
2029.630 Million cell updates/sec

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Perfect score: 482
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Fgapop 6.0 , Fgapext 7.0
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Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 2760536

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred. No.: 90

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3	460	95.4	90	9	US-09-872-185B-11
4	460	95.4	90	9	US-09-872-185B-12
5	460	95.4	90	15	US-10-666-513-3
6	460	95.4	90	16	US-10-665-867-3
7	460	95.4	90	16	US-10-665-867-4
8	319	66.2	92	14	US-10-077-600-2
9	319	66.2	92	16	US-10-755-889-334
10	230	47.7	50	9	US-09-826-589-2
11	230	47.7	50	9	US-09-872-185B-9
12	230	47.7	50	15	US-10-666-513-2
13	230	47.7	50	16	US-10-665-867-2
14	211.5	43.9	114	9	US-09-214-272-4
15	211.5	43.9	114	14	US-10-134-841-4
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17	211.5	43.9	114	15	US-10-116-275-225
18	211.5	43.9	114	15	US-10-131-410-146
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24	187	38.8	95	9	US-09-919-172-102
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29	180	37.3	92	10	US-09-919-039-184
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35	164.5	34.1	113	14	US-10-134-841-3
36	163	33.8	94	14	US-10-097-340-270
37	160	33.2	93	9	US-09-214-272-2
38	160	33.2	93	14	US-10-134-841-2
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40	160	33.2	93	16	US-10-624-631-31
41	160	33.2	93	16	US-10-755-889-328
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43	160	33.2	101	9	US-09-781-509-2
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45	160	33.2	119	13	US-10-087-192-1155

ALIGNMENTS

RESULT 1
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-3 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGGATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
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QY 64 GTGGGGCATTTTCGACACCCCTCAACAAGCTGAGCTGAAGCAGCTGATCACAAGGAACCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCCAAAACCCCTCCAGAACACCAAGATCAACCTTACCATTTGACAAAATATTCCAAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheHisGlnAspLeu 60

QY 184 GATCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTTCGTAGTCTGGTGTCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArgVal 80

QY 244 CTGAAAACAGCCCATAGATATCCACAAA 273
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RESULT 2
US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-4

Alignment Scores:
Pred. No.: 5.34e-45 Length: 90
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Percent Similarity: 100.00% Conservative: 0
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QY 64 GTGGGGCATTTTCGACACCCCTCAACAAGCTGAGCTGAAGCAGCTGATCACAAGGAACCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCCAAAACCCCTCCAGAACACCAAGATCAACCTTACCATTTGACAAAATATTCCAAGACCTG 183
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QY 184 GATCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTTCGTAGTCTGGTGTCCAGGGTG 243
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RESULT 3
US-09-872-185B-11
; Sequence 11, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-11

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 9 Gaps: 0

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QY 124 CCCAAAACCCCTCCAGAACACCAAGATCAACCTTACCATTTGACAAAATATTCCAAGACCTG 183
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RESULT 4
US-09-872-185B-12
; Sequence 12, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12

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; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-12

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Score:             460.00           Matches: 90
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QY      184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCcAGGGTG 243
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RESULT 5
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; Sequence 3, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAGE)
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
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US-10-666-513-3

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Db      21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY      124 CCcAAaACcCTCCAGaACACcCAaAGATCAACcCTACcATTGACAAaATATTCaAGACcCTG 183
Db      41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY      184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCcAGGGTG 243
Db      61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY      244 CTGAAaACAGCCcACATAGATATCCACAAa 273
Db      81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 6
US-10-665-867-3
; Sequence 3, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-3

Alignment Scores:
Pred. No.:          5.34e-45          Length: 90
Score:             460.00           Matches: 90
Percent Similarity: 100.00%          Conservative: 0
Best Local Similarity: 100.00%        Mismatches: 0
Query Match:       95.44%            Indels: 0
DB:                                                         Gaps: 0

US-09-910-208B-1 (1-276) x US-10-665-867-3 (1-90)

QY      4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCACCAGTACTCCGTTTCGG 63
Db      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY      64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACCTT 123
Db      21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY      124 CCcAAaACcCTCCAGaACACcCAaAGATCAACcCTACcATTGACAAaATATTCaAGACcCTG 183
Db      41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY      184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCcAGGGTG 243
Db      61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY      244 CTGAAaACAGCCcACATAGATATCCACAAa 273
Db      81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 7
US-10-665-867-4
; Sequence 4, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF

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; Sequence 2, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (47)..(47)
; OTHER INFORMATION: x=any amino acid
US-09-826-589-2

Alignment Scores:
Pred. No.:          4.45e-18          Length:          50
Score:              230.00           Matches:          46
Percent Similarity: 92.00%           Conservative:      0
Best Local Similarity: 92.00%         Mismatches:        4
Query Match:        47.72%           Indels:            0
DB:                  9               Gaps:              0

US-09-910-208B-1 (1-276) x US-09-826-589-2 (1-50)

Qy      4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
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Db      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIleGlyHisGlnTyrSerValArg 20

Qy      64 GTGGGGCATTTTCGACACCCCTCAACAAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
      |||||||
Db      21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40

Qy      124 CCCAAAACCCCTCCAGAACACCAAAAGATCAA 153
      |||||||
Db      41 ProLysThrLeuGlnAsn***LysAspGln 50

RESULT 11
US-10-666-513-2
; Sequence 9, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Bovine
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (47)..(47)
; OTHER INFORMATION: Where Xaa = unknown
US-09-872-185B-9

Alignment Scores:
Pred. No.:          4.45e-18          Length:          50
Score:              230.00           Matches:          46
Percent Similarity: 92.00%           Conservative:      0
Best Local Similarity: 92.00%         Mismatches:        4
Query Match:        47.72%           Indels:            0
DB:                  9               Gaps:              0

US-09-910-208B-1 (1-276) x US-09-826-589-2 (1-50)

Qy      4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
      |||||||
Db      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIleGlyHisGlnTyrSerValArg 20

Qy      64 GTGGGGCATTTTCGACACCCCTCAACAAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
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Db      21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40

Qy      124 CCCAAAACCCCTCCAGAACACCAAAAGATCAA 153
      |||||||
Db      41 ProLysThrLeuGlnAsn***LysAspGln 50

RESULT 12
US-10-666-513-2
; Sequence 2, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAG
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (47)
; OTHER INFORMATION: Xaa at this position is unknown
US-10-666-513-2

Alignment Scores:
Pred. No.:          4.45e-18          Length:          50
Score:              230.00           Matches:          46
Percent Similarity: 92.00%           Conservative:      0
Best Local Similarity: 92.00%         Mismatches:        4
Query Match:        47.72%           Indels:            0
DB:                  15              Gaps:              0

US-09-910-208B-1 (1-276) x US-10-666-513-2 (1-50)

Qy      4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
      |||||||
Db      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIleGlyHisGlnTyrSerValArg 20

Qy      64 GTGGGGCATTTTCGACACCCCTCAACAAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
      |||||||
Db      21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40

Qy      124 CCCAAAACCCCTCCAGAACACCAAAAGATCAA 153
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Db      41 ProLysThrLeuGlnAsn***LysAspGln 50

RESULT 13
US-10-665-867-2
; Sequence 2, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
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Best Local Similarity: 92.00%          Mismatches:          4
Query Match:          47.72%          Indels:              0
DB:                    9              Gaps:              0

US-09-910-208B-1 (1-276) x US-09-872-185B-9 (1-50)

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Db      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIleGlyHisGlnTyrSerValArg 20

Qy      64 GTGGGGCATTTTCGACACCCCTCAACAAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
      |||||||
Db      21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40

Qy      124 CCCAAAACCCCTCCAGAACACCAAAAGATCAA 153
      |||||||
Db      41 ProLysThrLeuGlnAsn***LysAspGln 50

RESULT 12
US-10-666-513-2
; Sequence 2, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAG
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (47)
; OTHER INFORMATION: Xaa at this position is unknown
US-10-666-513-2

Alignment Scores:
Pred. No.:          4.45e-18          Length:          50
Score:              230.00           Matches:          46
Percent Similarity: 92.00%           Conservative:      0
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Db      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIleGlyHisGlnTyrSerValArg 20

Qy      64 GTGGGGCATTTTCGACACCCCTCAACAAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
      |||||||
Db      21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40

Qy      124 CCCAAAACCCCTCCAGAACACCAAAAGATCAA 153
      |||||||
Db      41 ProLysThrLeuGlnAsn***LysAspGln 50

RESULT 13
US-10-665-867-2
; Sequence 2, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
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Q y	238	AGGGTGGCTGAAACACAGCCACATAGATATCCACAA	273
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D b	85	ArgLeuThrTrpAlaSerHisGluLysMethHisGlu	96

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Job time : 90 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:12:49 ; Search time 29.5 Seconds
(without alignments)
1396.823 Million cell updates/sec

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Perfect score: 482
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES									
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1	470	97.5	92	2	US-08-568-310D-19	Sequence 19, Appl			
2	470	97.5	92	3	US-09-270-455-19	Sequence 19, Appl			
3	460	95.4	90	4	US-09-263-312-3	Sequence 3, Appl			
4	460	95.4	90	4	US-09-826-589-3	Sequence 3, Appl			
5	460	95.4	90	4	US-09-826-589-4	Sequence 4, Appl			
6	371	77.0	91	3	US-08-794-000-2	Sequence 2, Appl			
7	371	77.0	91	4	US-09-646-651C-1	Sequence 1, Appl			
8	319	66.2	92	2	US-08-568-310D-20	Sequence 20, Appl			
9	319	66.2	92	3	US-09-270-455-20	Sequence 20, Appl			
10	266	55.2	51	2	US-08-568-310D-2	Sequence 2, Appl			
11	266	55.2	51	3	US-09-270-455-2	Sequence 2, Appl			
12	230	47.7	50	4	US-09-263-312-2	Sequence 2, Appl			

13	230	47.7	50	4	US-09-826-589-2	Sequence 2, Appli
14	211.5	43.9	114	1	US-08-385-241-3	Sequence 3, Appli
15	211.5	43.9	114	4	US-09-214-272-4	Sequence 4, Appli
16	211.5	43.9	114	4	US-09-806-382A-4	Sequence 4, Appli
17	204.5	42.4	109	1	US-07-987-272A-8	Sequence 8, Appli
18	190.5	39.5	113	2	US-08-918-727-7	Sequence 7, Appli
19	190.5	39.5	113	3	US-09-205-680A-7	Sequence 7, Appli
20	187	38.8	95	4	US-09-919-172-102	Sequence 102, App
21	187	38.8	95	4	US-09-976-594-467	Sequence 467, App
22	187	38.8	102	4	US-09-949-016-10557	Sequence 10557, A
23	184	38.2	92	2	US-09-051-589-1	Sequence 1, Appli
24	180	37.3	92	2	US-08-918-727-5	Sequence 5, Appli
25	180	37.3	92	3	US-09-205-680A-5	Sequence 5, Appli
26	180	37.3	92	4	US-09-919-039-184	Sequence 184, App
27	175	36.3	91	1	US-07-987-272A-11	Sequence 11, Appl
28	170	35.3	88	1	US-07-987-272A-1	Sequence 1, Appli
29	170	35.3	89	1	US-07-987-272A-14	Sequence 14, Appl
30	163	33.8	131	4	US-09-949-016-11241	Sequence 11241, A
31	160	33.2	31	2	US-08-568-310D-6	Sequence 6, Appli
32	160	33.2	31	3	US-09-270-455-6	Sequence 6, Appli
33	160	33.2	74	4	US-09-513-999C-5490	Sequence 5490, Ap
34	160	33.2	93	1	US-07-987-272A-7	Sequence 7, Appli
35	160	33.2	93	1	US-07-987-272A-16	Sequence 16, Appl
36	160	33.2	93	1	US-08-385-241-1	Sequence 1, Appli
37	160	33.2	93	4	US-09-214-272-2	Sequence 2, Appli
38	160	33.2	93	4	US-09-806-382A-3	Sequence 3, Appli
39	153	31.7	101	1	US-08-190-560-2	Sequence 2, Appli
40	153	31.7	101	1	US-08-469-277-2	Sequence 2, Appli
41	153	31.7	101	2	US-08-468-946-2	Sequence 2, Appli
42	153	31.7	101	2	US-08-468-942-2	Sequence 2, Appli
43	153	31.7	101	4	US-09-298-625-2	Sequence 2, Appli
44	145	30.1	75	1	US-07-987-272A-12	Sequence 12, Appl
45	144	29.9	76	1	US-07-987-272A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-568-310D-19
; Sequence 19, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92
US-08-568-310D-19

Alignment Scores:
Pred. No.: 3.95e-53 Length: 92
Score: 470.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.51% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-19 (1-92)

QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGGTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGlu 40

QY 121 CTTCCTCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 60

QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTTAGTCTCCTGGTGCCAGG 240
Db 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArg 80

QY 241 GTGCTGAAAACAGCCCATAGATATCCACAAAGAG 276
Db 81 ValLeuLysThrAlaHisIleAspIleHisLysGlu 92

RESULT 2
US-09-270-455-19
Sequence 19, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92
US-09-270-455-19

Alignment Scores:
Pred. No.: 3.95e-53 Length: 92
Score: 470.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.51% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-19 (1-92)

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Db 1 MetThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGGTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGlu 40

QY 121 CTTCCTCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 60

QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTTAGTCTCCTGGTGCCAGG 240
Db 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArg 80

QY 241 GTGCTGAAAACAGCCCATAGATATCCACAAAGAG 276
Db 81 ValLeuLysThrAlaHisIleAspIleHisLysGlu 92

RESULT 3
US-09-263-312-3
Sequence 3, Application US/09263312
Patent No. 6555340
GENERAL INFORMATION:
APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: Extracellular No. 6555340el RAGE Binding Protein (EN-RAGE) and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 0575/55873-A
CURRENT APPLICATION NUMBER: US/09/263,312
CURRENT FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 90
TYPE: PRT
ORGANISM: Human
US-09-263-312-3

Alignment Scores:

Pred. No.: 8.06e-52 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-263-312-3 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 GTGGGGCATTTTCGACACCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCCAAAACCTCCAGAACCAAGATCAACCTACCATTTGACAAAATATTTCCAAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCCGATAAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCCTGTTCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAAAACAGCCCATAGATATCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 4
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Alignment Scores:
Pred. No.: 8.06e-52 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-3 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 GTGGGGCATTTTCGACACCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCCAAAACCTCCAGAACCAAGATCAACCTACCATTTGACAAAATATTTCCAAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCCGATAAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCCTGTTCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAAAACAGCCCATAGATATCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 4
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Alignment Scores:
Pred. No.: 8.06e-52 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 4 Gaps: 0

QY 244 CTGAAAACAGCCCATAGATATCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 5
US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-4

Alignment Scores:
Pred. No.: 8.06e-52 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-4 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 GTGGGGCATTTTCGACACCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCCAAAACCTCCAGAACCAAGATCAACCTACCATTTGACAAAATATTTCCAAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCCGATAAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCCTGTTCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAAAACAGCCCATAGATATCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 6
US-08-794-000-2
; Sequence 2, Application US/08794000
; Patent No. 6087123
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Metal-Containing Ribonucleotide Polypeptides
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,000
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DE96/01337
; FILING DATE: 17-JUL-1996

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 25 992.0
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 30 500.0
; FILING DATE: 18-AUG-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-794-000-2

Alignment Scores:
Pred. No.: 4.02e-40 Length: 91
Score: 371.00 Matches: 74
Percent Similarity: 91.21% Conservative: 9
Best Local Similarity: 81.32% Mismatches: 8
Query Match: 76.97% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-794-000-2 (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAAACCTCCAGAACACCAAGATCAACCTACCATTCGACAAAATATTTCCAGACCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
QY 184 GATGCCGATAAAGACCGAGCCGTGAGCTTTGAGGAATTCGTAGTCCTCCTAGGTTG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80

QY 244 CTGAAAACAGCCCATAGATATCCACAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 7
US-09-646-651C-1
; Sequence 1, Application US/09646651C
; Patent No. 6770455
; GENERAL INFORMATION:
; APPLICANT: Kiesewetter, Stefan
; APPLICANT: Kuhn, Eckehard
; APPLICANT: Koch-Pelster, Brigitte
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
; FILE REFERENCE: 206579
; CURRENT APPLICATION NUMBER: US/09/646,651C
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/EP98/07722
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: DE 198 11 047.2
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..{}
; OTHER INFORMATION: Angiotropin-related protein
US-09-646-651C-1
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;
; Alignment Scores:
; Pred. No.: 4.02e-40 Length: 91
; Score: 371.00 Matches: 74
; Percent Similarity: 91.21% Conservative: 9
; Best Local Similarity: 81.32% Mismatches: 8
; Query Match: 76.97% Indels: 0
; DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-646-651C-1 (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAAACCTCCAGAACACCAAGATCAACCTACCATTCGACAAAATATTTCCAGACCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
QY 184 GATGCCGATAAAGACCGAGCCGTGAGCTTTGAGGAATTCGTAGTCCTCCTAGGTTG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80

QY 244 CTGAAAACAGCCCATAGATATCCACAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 8
US-08-568-310D-20
; Sequence 20, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 20:
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-20

Alignment Scores:
Pred. No.: 2.75e-33 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservatve: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-20 (1-92)
QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCCTCCAAAACCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTTCGTAGTCTCGTGTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCACATAGATATCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 9
US-09-270-455-20
; Sequence 20, Application US/09270455
; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,455
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/568,310
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON

; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 20: FROM 1 TO 92
US-09-270-455-20

Alignment Scores:
Pred. No.: 2.75e-33 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservatve: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-20 (1-92)
QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCCTCCAAAACCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTTCGTAGTCTCGTGTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCACATAGATATCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10
US-08-568-310D-2
; Sequence 2, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D

/ FILING DATE: DECEMBER 6, 1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/568,310
/ FILING DATE: 7-70468 and 7-45564 (both Japan)
/ FILING DATE: 3/6/95 and 3/6/95, respectively
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KLEIN, MILTON
/ REGISTRATION NUMBER: 27101
/ REFERENCE/DOCKET NUMBER: 3316
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)953-3350
/ TELEFAX: (212)953-3352
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 51
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ PUBLICATION INFORMATION:
/ RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51
/ RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 51
US-08-568-310D-2

Alignment Scores:
Pred. No.: 2.03e-26 Length: 51
Score: 266.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.19% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-2 (1-51)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACAGTACTCCGTTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACCT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACCT 156
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnPro 51

RESULT 11
US-09-270-455-2
/ Sequence 2, Application US/09270455
/ Patent No. 6313267
/ GENERAL INFORMATION:
/ APPLICANT: HITOMI, JIRO
/ APPLICANT: YAMAGUCHI, KEN
/ APPLICANT: YAMAMURA, TOKUJIRO
/ APPLICANT: KIMURA, TATSUJI
/ TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
/ STREET: 99 PARK AVENUE
/ STREET: 6th FLOOR
/ CITY: NEW YORK CITY
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10016
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
/ MEDIUM TYPE: STORAGE
/ COMPUTER: IBM-PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS 6.2
/ SOFTWARE: WORDPERFECT 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/270,455
/ FILING DATE:

/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/568,310
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KLEIN, MILTON
/ REGISTRATION NUMBER: 27101
/ REFERENCE/DOCKET NUMBER: 3316
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)953-3350
/ TELEFAX: (212)953-3352
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 51
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ PUBLICATION INFORMATION:
/ RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51
US-09-270-455-2

Alignment Scores:
Pred. No.: 2.03e-26 Length: 51
Score: 266.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.19% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-2 (1-51)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACAGTACTCCGTTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACCT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACCT 156
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnPro 51

RESULT 12
US-09-263-312-2
/ Sequence 2, Application US/09263312
/ Patent No. 6555340
/ GENERAL INFORMATION:
/ APPLICANT: Schmidt, Ann Marie
/ APPLICANT: Stern, David
/ TITLE OF INVENTION: Extracellular No. 6555340el RAGE Binding Protein (EN-RAGE) and
/ TITLE OF INVENTION: Uses Thereof
/ FILE REFERENCE: 0575/55873-A
/ CURRENT APPLICATION NUMBER: US/09/263,312
/ CURRENT FILING DATE: 1999-03-05
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 50
/ TYPE: PRT
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (47)
/ OTHER INFORMATION: Xaa at this position is unknown
US-09-263-312-2

Alignment Scores:
Pred. No.: 1.08e-21 Length: 50
Score: 230.00 Matches: 46
Percent Similarity: 92.00% Conservative: 0
Best Local Similarity: 92.00% Mismatches: 4
Query Match: 47.72% Indels: 0

DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-263-312-2 (1-50)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
|||||
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIleGlyHisGlnTyrSerValArg 20

QY 64 GTGGGCGATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
|||||
Db 21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40

QY 124 CCCAAACCTCCAGAACACCAAGATCAA 153
|||||
Db 41 ProlysThrLeuGlnAsn**LysAspGln 50

RESULT 13

US-09-826-589-2

; Sequence 2, Application US/09826589

; Patent No. 6670136

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Stern, David

; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE

; FILE REFERENCE: 0575/55873-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/826,589

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 50

; TYPE: PRT

; ORGANISM: Human

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (47)..(47)

; OTHER INFORMATION: x=any amino acid

US-09-826-589-2

Alignment Scores:

Pred. No.: 1.08e-21 Length: 50

Score: 230.00 Matches: 46

Percent Similarity: 92.00% Conservative: 0

Best Local Similarity: 92.00% Mismatches: 4

Query Match: 47.72% Indels: 0

DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-2 (1-50)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
|||||
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIleGlyHisGlnTyrSerValArg 20

QY 64 GTGGGCGATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
|||||
Db 21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40

QY 124 CCCAAACCTCCAGAACACCAAGATCAA 153
|||||
Db 41 ProlysThrLeuGlnAsn**LysAspGln 50

RESULT 14

US-08-385-241-3

; Sequence 3, Application US/08385241

; Patent No. 5776348

; GENERAL INFORMATION:

; APPLICANT: Selengut Ph.D., Jeremy D.

; APPLICANT: Orme-Johnson Ph.D., William H.

; APPLICANT: Dretler M.D., Stephen P.

; APPLICANT: Asakura M.D., Hirotaka

; TITLE OF INVENTION: SYSTEM AND METHOD FOR INHIBITING

; TITLE OF INVENTION: FORMATION OF CRYSTALLINE STRUCTURES THAT INCLUDE STRUVITE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Choate, Hall & Stewart

; STREET: 53 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2891

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/385,241

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Herschbach Ph.D., Brenda M.

; REGISTRATION NUMBER: P-39,223

; REFERENCE/DOCKET NUMBER: 492611-000 (MIT6915)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-5175

; TELEFAX: (617) 248-4000

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 114 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; IMMEDIATE SOURCE:

; CLONE: hMRP-14 protein

US-08-385-241-3

Alignment Scores:

Pred. No.: 3.98e-19 Length: 114

Score: 211.50 Matches: 41

Percent Similarity: 71.74% Conservative: 25

Best Local Similarity: 44.57% Mismatches: 25

Query Match: 43.88% Indels: 1

DB: 1 Gaps: 1

US-09-910-208B-1 (1-276) x US-08-385-241-3 (1-114)

QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
|||||
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleIleAsnThrPheHisGlnTyrSerVal 24

QY 61 CGGGTGGGCGATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAA 120
|||||
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44

QY 121 CTTCCCAAAACCCCTC---CAGAACACCAAGATCAACCTACCATTGACAAAATATTTCCAA 177
|||||
Db 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64

QY 178 GACCTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGTGTCC 237
|||||
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84

QY 238 AGGGTGTGAAACAGCCCATAGATATCCACAAA 273
|||||
Db 85 ArgLeuThrTrpAlaSerHisGluLysMethHisGlu 96

RESULT 15

US-09-214-272-4

; Sequence 4, Application US/09214272

; Patent No. 6620790

; GENERAL INFORMATION:

; APPLICANT: Siegenthaler, Georges

; TITLE OF INVENTION: Isolated Arachidonic Acid-Binding Heteromer and its Use in

; TITLE OF INVENTION: Cosmetics and Pharmaceuticals
; FILE REFERENCE: 016800-254
; CURRENT APPLICATION NUMBER: US/09/214,272
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: PCT/FR97/01164
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: FR 96/08219
; PRIOR FILING DATE: 1996-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of MRP-14.
US-09-214-272-4

Alignment Scores:
Pred. No.: 3.98e-19 Length: 114
Score: 211.50 Matches: 41
Percent Similarity: 71.74% Conservative: 25
Best Local Similarity: 44.57% Mismatches: 25
Query Match: 43.88% Indels: 1
DB: 4 Gaps: 1

US-09-910-208B-1 (1-276) x US-09-214-272-4 (1-114)

QY	1	ATGACTAAGCTGGAGATCATCCTGGAGGAGATCATCAACATCTTCCACCAGTACTCCGTT	60
Db	5	MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTyrSerVal	24
QY	61	CGGTGGGGCATTTCGACACCCCTCAACAAGCTGAGCTGAAGCAGCTGATCACAAGGAA	120
Db	25	LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp	44
QY	121	CTTCCCAAAACCCTC---CAGAACACCAAGATCAACCTACCATTCACAAAATATCCAA	177
Db	45	LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu	64
QY	178	GACCTGGATGCCGATAAAGACGGAGCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTC	237
Db	65	AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla	84
QY	238	AGGTGCTGAAACAGCCACATAGATATCCACAA	273
Db	85	ArgLeuThrTrpAlaSerHisGluLysMethHisGlu	96

Search completed: February 23, 2005, 11:24:52
Job time : 30.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: February 23, 2005, 11:25:01 ; Search time 27 Seconds
(without alignments)
1967.098 Million cell updates/sec

Title: US-09-910-208B-1
Perfect score: 92
Sequence: 1 atgactaagctggaagatca.....acatagatatccacaagag 276

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Word size: 1
Total number of Hits satisfying chosen parameters: 565918

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

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-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	21.7	91	A55406	calgranulin c - pi
2	11	12.0	122	A42628	calgranulin B - bo
3	9	9.8	92	JC4712	S-100 calcium-bind
C 4	8	8.7	72	T12854	hypothetical prote
5	8	8.7	275	T22414	hypothetical prote
C 6	8	8.7	334	G71228	hypothetical prote
C 7	8	8.7	363	AF2375	hypothetical prote
8	8	8.7	725	A41258	a-agglutinin core
9	8	8.7	819	T19351	hypothetical prote
C 10	7	7.6	41	B41655	sucrose catabolism
11	7	7.6	57	AH2906	conserved hypothet
C 12	7	7.6	78	T03670	reverse transcript
C 13	7	7.6	81	T03707	reverse transcript
C 14	7	7.6	81	T06548	RNA-directed DNA p

reverse transcript	81	2	T03937
RNA-directed DNA p	81	2	T09158
retrovirus-related	88	2	B47758
reverse transcript	92	2	T03665
parvalbumin beta -	109	1	PVSNBB
hypothetical prote	114	2	T23119
hypothetical prote	127	2	AG2241
export protein xps	138	2	S17941
hypothetical prote	141	2	G71079
pol polyprotein -	193	2	A33562
hypothetical prote	208	2	T15790
insulin receptor -	210	2	I55609
adenylate kinase (212	2	B97898
hypothetical prote	219	2	T51074
hypothetical prote	236	2	B84718
phosphatidate cyti	249	1	SYECDG
CDP-diglyceride sy	249	2	A99651
CDP-diglyceride sy	249	2	A85502
centromere-like fu	253	2	B84157
1-acylglycerol-3-p	255	2	S70545
1-acyl-sn-glycerol	255	2	A81099
1-acylglycerol-3-p	255	2	A81842
1-acylglycerol-3-p	257	2	S70544
hypothetical prote	261	2	A99421
hypothetical prote	264	2	T05594
hypothetical prote	272	2	T01480
hypothetical prote	281	2	T49537
hypothetical prote	285	2	S08491
hypothetical prote	292	2	S24169
mucin - rat	293	2	H70067
transcription regu	299	2	T26789
hypothetical prote	306	2	D89841
fructose 1-phospha	309	2	E86779
hypothetical prote	313	2	A57499
N5-(carboxyethyl)o	314	2	H69458
potassium channel	318	2	B82447
conserved hypothet	330	2	C95844
probable sugar ABC	332	2	S60935
hypothetical prote	334	2	C87272
ABC transporter, A	342	2	S51402
probable membrane	344	2	D75486
probable UDP-glucu	344	2	G96599
protein F14J16.8 (373	2	S43455
hypothetical prote	376	2	S52137
MID2 protein - yea	379	2	AB2423
hypothetical prote	384	2	G83607
polyamine transpor	387	2	C71827
hypothetical prote	393	2	D75511
hypothetical prote	394	2	B70411
fimbrial assembly	399	2	E86348
F14J8.16 protein -	402	2	S47329
OXA1 protein precu	407	2	T36979
probable integral	410	2	AH1484
probable cell surf	421	2	C70038
maltose/maltodextr	426	2	T45767
hypothetical prote	434	2	D96716
probable alpha/bet	438	2	B83017
probable MFS trans	472	2	T08860
hypothetical prote	473	2	B84556
4-hydroxybutyrate	474	2	E69481
probable membrane	475	2	S49886
periplasmic sorbit	475	2	G98183
4-hydroxybutyrate	482	2	H69392
hypothetical prote	488	2	T19854
probable signaling	504	2	A84244
sucrose porin scry	505	2	A39127
probable porin scry	505	2	S15193
probable exonuclea	506	2	F96772
PTS system, (possi	518	2	H97320
hypothetical prote	518	2	T49778
ASM4 protein - yea	528	2	S67624
laccase (EC 1.10.3	529	2	S49120
related to COP1-in	532	2	T49467

88	7	7.6	533	2	S62371	laccase (EC 1.10.3	c 161	6	6.5	88	2	I47759	retrovirus-related
89	7	7.6	543	2	S35047	mucin JUL7 - human	c 162	6	6.5	88	2	D47759	retrovirus-related
90	7	7.6	547	2	A48442	membrane transport	c 163	6	6.5	88	2	B47760	retrovirus-related
91	7	7.6	548	2	T49948	hypothetical prote	c 164	6	6.5	88	2	D90957	hypothetical prote
c 92	7	7.6	556	2	T16790	hypothetical prote	c 165	6	6.5	88	2	D56084	interleukin-lbeta
93	7	7.6	560	2	AB2220	hypothetical prote	166	6	6.5	88	2	B83933	hypothetical prote
94	7	7.6	602	2	S58336	probable membrane	167	6	6.5	89	2	E47758	retrovirus-related
95	7	7.6	610	2	S35049	mucin JER57 - huma	c 168	6	6.5	90	2	G72240	hypothetical prote
c 96	7	7.6	616	2	AE1973	serine/threonine k	169	6	6.5	91	2	T07178	hypothetical prote
97	7	7.6	635	2	T00011	ccal protein - rat	170	6	6.5	93	2	B41609	hypothetical prote
c 98	7	7.6	641	2	E96612	probable transcrip	171	6	6.5	95	1	S35985	hlpA protein - Cry
99	7	7.6	647	2	S26386	transcription fact	172	6	6.5	95	2	G84548	S-100 protein alph
c 100	7	7.6	675	2	S74399	sensory transducti	173	6	6.5	95	2	T18004	hypothetical prote
101	7	7.6	687	2	A40711	RNA polymerase II	174	6	6.5	97	2	JC7322	hypothetical prote
102	7	7.6	703	2	T48019	hypothetical prote	175	6	6.5	100	2	F69133	deafness dystonia
103	7	7.6	729	2	T35028	probable glycosyl	176	6	6.5	100	2	C71012	ribosomal protein
104	7	7.6	775	2	A83936	stage V sporulatio	c 177	6	6.5	100	2	T49857	hypothetical prote
105	7	7.6	776	1	S44047	glucocorticoid rec	178	6	6.5	101	2	D69395	H+-transporting AT
106	7	7.6	794	2	F85040	hypothetical prote	c 179	6	6.5	101	2	F82797	hypothetical prote
107	7	7.6	796	2	T21460	hypothetical prote	180	6	6.5	103	2	T03148	hypothetical prote
108	7	7.6	845	2	T52518	related to cytosin	181	6	6.5	105	1	W7WL18	hypothetical prote
c 109	7	7.6	849	2	S37350	luxN protein - Vib	c 182	6	6.5	105	2	G95911	E7 protein - human
110	7	7.6	859	2	S51646	inscuteable protei	183	6	6.5	106	1	QQBPP4	probable ferredoxi
111	7	7.6	877	2	S49783	probable membrane	184	6	6.5	106	2	B41830	orf-106 protein -
c 112	7	7.6	902	1	S54495	probable carrier p	185	6	6.5	106	2	AD1063	DNA replication pr
113	7	7.6	982	2	T13653	hypothetical prote	c 186	6	6.5	107	2	A72456	hypothetical P4 ph
114	7	7.6	1023	2	E71376	conserved hypotet	c 187	6	6.5	107	2	KVMS49	hypothetical prote
115	7	7.6	1098	2	T50364	hypothetical prote	c 188	6	6.5	108	2	AF1935	Ig kappa chain V r
116	7	7.6	1123	2	AB0125	exodeoxyribonuclea	189	6	6.5	108	2	C97824	hypothetical prote
117	7	7.6	1129	2	T19779	hypothetical prote	c 189	6	6.5	109	2	G71249	S0S ribosomal prot
118	7	7.6	1161	2	S18738	pol protein - simi	c 190	6	6.5	109	2	G69609	cytochrome-c oxida
119	7	7.6	1338	2	T18287	protein-tyrosine k	c 191	6	6.5	110	2	B72713	hypothetical prote
120	7	7.6	1339	2	T40245	probable transcrip	c 192	6	6.5	110	2	E72683	hypothetical prote
c 121	7	7.6	1463	2	T30290	AAS surface protei	c 193	6	6.5	111	2	AC1648	hypothetical prote
122	7	7.6	1659	2	T15666	hypothetical prote	c 194	6	6.5	111	2	A85906	probable ybhH sigm
123	7	7.6	1726	2	T30810	chromatin structur	c 195	6	6.5	113	2	D91061	probable ybhH sigm
124	7	7.6	2055	2	T30259	multiple PDZ domai	c 196	6	6.5	113	2	Q5ECPA	probable ybhH sigm
125	7	7.6	2163	2	S50675	pre-mRNA splicing	c 197	6	6.5	114	1	B31848	calgranulin B [val
126	7	7.6	2164	1	GNNY89	genome polyprotein	198	6	6.5	114	2	S75565	hypothetical prote
c 127	7	7.6	2182	2	T28634	variant-specific s	199	6	6.5	116	2	G95167	IS66 family elemen
128	7	7.6	2285	2	T12796	probable transglyc	200	6	6.5	116	2	A99034	degenerate transpo
129	7	7.6	3570	2	T45025	mucin MUC5B, trach	c 201	6	6.5	116	2	S12685	hypothetical prote
130	7	7.6	7829	2	T15789	hypothetical prote	c 202	6	6.5	116	2	F90024	hypothetical prote
131	6	6.5	20	2	S18582	hypothetical prote	203	6	6.5	117	2	T49382	hypothetical prote
132	6	6.5	20	2	T50757	pufK protein [impo	c 204	6	6.5	120	2	H81728	conserved hypotet
133	6	6.5	29	2	S01448	hypothetical prote	c 205	6	6.5	121	2	B82244	response regulator
c 134	6	6.5	34	2	F81919	hypothetical prote	c 206	6	6.5	122	2	B33959	heat-labile entero
135	6	6.5	38	2	I46861	macrophage migrati	c 207	6	6.5	123	2	C98103	ribonuclease P (EC
c 136	6	6.5	39	2	I40555	rap60B protein - B	c 208	6	6.5	123	2	B95239	ribonuclease P pro
c 137	6	6.5	46	1	S66584	hypothetical prote	c 209	6	6.5	123	2	T38675	DNA-directed RNA p
c 138	6	6.5	46	1	S66591	hypothetical prote	c 210	6	6.5	124	2	S40348	Ig kappa chain V-J
139	6	6.5	46	2	PC4400	crotoxin-binding p	c 211	6	6.5	125	2	AC1862	hypothetical prote
c 140	6	6.5	47	2	E89810	hypothetical prote	c 212	6	6.5	126	2	A70886	hypothetical prote
141	6	6.5	52	2	A81042	conserved hypotet	c 213	6	6.5	126	2	S76349	hypothetical prote
c 142	6	6.5	53	2	G70246	hypothetical prote	c 214	6	6.5	127	2	C95887	probable translati
c 143	6	6.5	55	2	E91155	hypothetical prote	c 215	6	6.5	128	2	B28183	beta-lactamase rep
c 144	6	6.5	55	2	B86001	hypothetical prote	c 216	6	6.5	129	2	S76962	hypothetical prote
c 145	6	6.5	55	2	JV0064	hypothetical 6K pr	c 217	6	6.5	130	2	A69216	translation initia
146	6	6.5	56	2	AF0385	hypothetical prote	c 218	6	6.5	130	2	E83532	hypothetical prote
147	6	6.5	61	2	C69260	hypothetical prote	c 219	6	6.5	130	2	F70908	hypothetical prote
148	6	6.5	71	1	IHPC	high potential iro	c 220	6	6.5	131	2	T11570	hypothetical prote
c 149	6	6.5	72	2	T07369	ubiquinol-cytochro	c 221	6	6.5	131	2	D70474	hypothetical prote
150	6	6.5	74	2	T18183	hypothetical prote	c 222	6	6.5	133	2	AB2502	hypothetical prote
151	6	6.5	79	1	JN0246	calcium-binding pr	c 223	6	6.5	134	2	PC4252	natriuretic peptid
152	6	6.5	79	1	KLBOI	calcium-binding pr	c 224	6	6.5	135	1	A61244	hypothetical 135 p
153	6	6.5	79	1	KLPGI	calcium-binding pr	225	6	6.5	135	2	F86239	protein F20B24.4 l
c 154	6	6.5	81	2	T10743	RNA-directed DNA p	226	6	6.5	135	2	E75347	hypothetical prote
c 155	6	6.5	82	2	D82577	hypothetical prote	c 227	6	6.5	138	2	T33495	hypothetical prote
c 156	6	6.5	82	2	AH2065	hypothetical prote	c 228	6	6.5	138	2	AD0368	probable membrane
157	6	6.5	84	2	D83423	hypothetical prote	c 229	6	6.5	139	2	H89287	protein par-1 [imp
158	6	6.5	84	2	AI3563	hypothetical prote	c 230	6	6.5	139	2	H87305	phosphoribosyl-AMP
159	6	6.5	84	2	AD2158	hypothetical prote	c 231	6	6.5	139	2	AC1418	B. subtilis stress
c 160	6	6.5	87	2	H84234	hypothetical prote	232	6	6.5	139	2	AE1793	B. subtilis stress
							233	6	6.5				

C 234	6	6.5	140	2	C69963	conserved hypothet	307	6	6.5	183	2	F75086	hypothetical prote
235	6	6.5	145	2	AG3166	hypothetical prote	308	6	6.5	183	2	T25102	hypothetical prote
C 236	6	6.5	146	2	T51473	calmodulin-like pr	C 309	6	6.5	183	2	S70307	hypothetical prote
C 237	6	6.5	146	2	G71181	hypothetical prote	C 310	6	6.5	183	2	C97017	probable membrane
C 238	6	6.5	147	1	G65063	hypothetical prote	C 311	6	6.5	184	2	T06673	response reactor 2
239	6	6.5	147	2	I46467	luteinizing hormon	C 312	6	6.5	184	2	T50855	two-component resp
C 240	6	6.5	147	2	AC0864	conserved hypothet	C 313	6	6.5	184	2	T50856	response regulator
C 241	6	6.5	147	2	A85933	hypothetical prote	C 314	6	6.5	186	2	T50857	response regulator
C 242	6	6.5	147	2	G91087	hypothetical prote	315	6	6.5	187	2	E87299	hypothetical prote
C 243	6	6.5	148	2	F86701	hypothetical prote	C 316	6	6.5	189	2	F82969	hypothetical prote
244	6	6.5	148	2	G64466	hypothetical prote	317	6	6.5	190	2	S66981	ribosomal protein
245	6	6.5	149	2	B48083	chromosome segrega	C 318	6	6.5	190	2	S52729	ribosomal protein
C 246	6	6.5	149	2	E83088	hypothetical prote	C 319	6	6.5	191	2	H87330	hypothetical prote
C 247	6	6.5	149	2	JC4983	hypothetical 17.1K	320	6	6.5	192	2	T12775	hypothetical yokK
C 248	6	6.5	149	2	A95105	conserved hypothet	321	6	6.5	192	2	S52249	response regulator
C 249	6	6.5	149	2	A97973	conserved hypothet	C 322	6	6.5	193	2	E95340	hypothetical prote
C 250	6	6.5	150	2	S42203	avidin-related pro	C 323	6	6.5	194	2	D87648	conserved hypothet
C 251	6	6.5	150	2	S42202	avidin-related pro	C 324	6	6.5	194	2	T46920	hypothetical prote
C 252	6	6.5	150	2	S42204	avidin-related pro	C 325	6	6.5	195	2	I40573	flagellin chain A
C 253	6	6.5	150	2	T44952	flagella-related p	C 326	6	6.5	195	2	QBED6	HRF6 protein - hu
C 254	6	6.5	150	2	S37018	transposase (clone	327	6	6.5	197	1	B95309	probable ABC sugar
C 255	6	6.5	151	2	JC2321	hypothetical 17.0K	C 328	6	6.5	197	2	AF1870	hypothetical prote
256	6	6.5	151	2	T32957	hypothetical prote	C 329	6	6.5	198	2	AC2792	conserved hypothet
C 257	6	6.5	151	2	A64038	hypothetical prote	C 330	6	6.5	199	2	B70516	hypothetical prote
C 258	6	6.5	151	2	S75732	hypothetical prote	C 331	6	6.5	201	2	S72806	hypothetical prote
C 259	6	6.5	152	2	S31002	gene 57 protein -	332	6	6.5	202	2	T30927	hypothetical prote
C 260	6	6.5	153	2	T29391	hypothetical prote	333	6	6.5	202	2	AB2378	hypothetical prote
261	6	6.5	153	2	S67294	hypothetical prote	C 334	6	6.5	203	2	S53587	probable membrane
C 262	6	6.5	155	2	T25845	hypothetical prote	335	6	6.5	203	2	T33864	hypothetical prote
C 263	6	6.5	155	2	AE0333	hypothetical prote	C 336	6	6.5	203	2	T25222	hypothetical prote
C 264	6	6.5	156	2	H72621	probable exported	C 337	6	6.5	204	2	B85879	hypothetical prote
C 265	6	6.5	157	2	H72065	hypothetical prote	C 338	6	6.5	204	2	H91034	probable positive
C 266	6	6.5	160	2	S76609	ribosomal protein	C 339	6	6.5	204	2	JU0220	probable positive
267	6	6.5	160	2	AE0135	hypothetical prote	C 340	6	6.5	209	2	S65767	hypothetical prote
C 268	6	6.5	160	2	A97496	Ssra-binding prote	C 341	6	6.5	209	2	S65768	hypothetical prote
C 269	6	6.5	160	2	AD2714	probable extracell	C 342	6	6.5	209	2	T37785	hypothetical prote
270	6	6.5	161	2	B64106	conserved hypothet	343	6	6.5	210	2	H72585	hypothetical prote
C 271	6	6.5	161	2	C84235	small protein smpB	344	6	6.5	211	2	T25237	hypothetical prote
272	6	6.5	161	2	H72571	hypothetical prote	345	6	6.5	211	2	D90065	hypothetical prote
273	6	6.5	161	2	A97805	hypothetical prote	346	6	6.5	213	2	F86310	hypothetical prote
C 274	6	6.5	162	2	T50860	response regulator	347	6	6.5	214	2	T13011	protein F1L3.8 lim
C 275	6	6.5	163	2	E97908	hypothetical prote	348	6	6.5	215	1	QBEF3	hypothetical prote
C 276	6	6.5	163	2	B95038	hypothetical prote	C 349	6	6.5	215	2	D91177	HXLFI protein prec
C 277	6	6.5	164	2	S43226	PTS system, IIB co	C 350	6	6.5	215	2	S47728	probable transport
C 278	6	6.5	165	2	S01510	homeotic protein P	C 351	6	6.5	215	2	E86023	probable transport
279	6	6.5	165	2	T38202	NADH2 dehydrogenas	C 352	6	6.5	215	2	S23432	pyroglutamyl-pepti
C 280	6	6.5	165	2	A95161	hypothetical serin	C 353	6	6.5	215	2	C70471	hypothetical prote
C 281	6	6.5	165	2	H98026	conserved hypothet	354	6	6.5	216	2	B97926	conserved hypothet
C 282	6	6.5	166	2	C86559	S7 ribosomal prote	355	6	6.5	216	2	S05586	hypothetical prote
C 283	6	6.5	166	2	C72734	hypothetical prote	356	6	6.5	216	2	F95056	PAP2 family protei
284	6	6.5	167	2	A87150	hypothetical prote	357	6	6.5	217	2	AF0906	conserved hypothet
C 285	6	6.5	168	2	E84362	tuberculin related	358	6	6.5	217	2	E70574	probable transcrip
C 286	6	6.5	170	2	S56958	GRP cyclohydrolase	359	6	6.5	217	2	AB3476	hypothetical prote
C 287	6	6.5	172	2	G91049	probable membrane	360	6	6.5	218	2	S32965	probable GTP-bindi
C 288	6	6.5	172	2	D85894	probable outer mem	C 361	6	6.5	218	2	T02384	hypothetical prote
C 289	6	6.5	172	2	H65026	probable outer mem	C 362	6	6.5	219	2	C97571	hypothetical prote
C 290	6	6.5	174	2	S68246	hypothetical prote	C 363	6	6.5	220	2	D70450	phosphoglycerate m
C 291	6	6.5	175	2	H90768	phosphatidylcholin	364	6	6.5	220	2	S20064	ribosomal protein
292	6	6.5	175	2	AE2486	probable copper/zi	365	6	6.5	220	2	C65112	sigma cross-reacti
C 293	6	6.5	175	2	A71358	aminoglycoside ade	366	6	6.5	220	2	H91139	sigma cross-reacti
294	6	6.5	175	2	E82118	hypothetical prote	367	6	6.5	220	2	C85985	sigma cross-reacti
C 295	6	6.5	175	2	G71480	conserved hypothet	C 368	6	6.5	220	2	E87053	conserved hypothet
296	6	6.5	175	2	B42463	hypothetical prote	C 369	6	6.5	221	2	AI0089	probable flagellar
297	6	6.5	175	2	C42291	tail fiber assembl	370	6	6.5	222	2	A27270	myosin light chain
298	6	6.5	175	2	I38408	neu differentiatio	C 371	6	6.5	222	2	H87496	hypothetical prote
C 299	6	6.5	177	2	B84186	inorganic pyrophos	C 372	6	6.5	224	2	T51875	hypothetical prote
C 300	6	6.5	177	2	G72457	hypothetical prote	C 373	6	6.5	225	1	ADPSGP	2-dehydro-3-deoxy-
301	6	6.5	178	2	A49014	20K protein - rabb	C 374	6	6.5	225	2	C88633	protein F56B3.3 li
302	6	6.5	178	2	T42661	hypothetical prote	375	6	6.5	226	2	B64500	ribose-5-phosphate
C 303	6	6.5	179	2	F97683	50S ribosomal prot	C 376	6	6.5	226	2	D70540	probable dethiobio
C 304	6	6.5	179	2	AF2908	50S ribosomal prot	C 377	6	6.5	226	2	E70769	hypothetical prote
C 305	6	6.5	179	2	B70757	hypothetical prote	C 378	6	6.5	227	2	A47635	MHC class II histo
C 306	6	6.5	182	2	AG1508	protein involved i	379	6	6.5	227	2	T03807	hypothetical prote

c 380 6 6.5 227 2 T02413 probable RING zinc
c 381 6 6.5 227 2 C89839 conserved hypothet
c 382 6 6.5 228 2 A53271 MHC class II histo
c 383 6 6.5 228 2 E87612 cytochrome c, memb
c 384 6 6.5 228 2 H97336 uncharacterized co
c 385 6 6.5 229 1 F75267 probable cytochrom
c 386 6 6.5 229 2 S30486 hypothetical 25.6K
c 387 6 6.5 229 2 AG2390 hypothetical prote
c 388 6 6.5 230 2 S14686 hypothetical prote
c 389 6 6.5 230 2 A56210 neu differentiatio
c 390 6 6.5 231 2 T50827 superoxide dismuta
c 391 6 6.5 233 2 AB2107 hypothetical prote
c 392 6 6.5 234 2 C83587 hypothetical prote
c 393 6 6.5 234 2 E96957 HAD superfamily hy
c 394 6 6.5 234 2 D96932 ABC transporter, A
c 395 6 6.5 235 2 T42096 ATP-dependent Clp
c 396 6 6.5 235 2 S51813 photosystem-I PSI-
c 397 6 6.5 235 2 T03139 hypothetical prote
c 398 6 6.5 236 2 T36399 probable alcohol d
c 399 6 6.5 236 2 T06462 Glutathione peroxi
c 400 6 6.5 237 2 H69820 conserved hypothet
c 401 6 6.5 237 2 T01359 fatty acid hydroxy
c 402 6 6.5 238 2 T07921 probable starch sy
c 403 6 6.5 238 2 E64416 hypothetical prote
c 404 6 6.5 238 2 G64117 nifs protein homol
c 405 6 6.5 239 2 B70465 probable export pr
c 406 6 6.5 239 2 C65222 probable 2-compone
c 407 6 6.5 239 2 B91267 two-component tran
c 408 6 6.5 239 2 G86107 probable 2-compone
c 409 6 6.5 240 2 AF0570 fimbriae Y protein
c 410 6 6.5 240 2 A45273 fimA expression re
c 411 6 6.5 240 2 H69846 hypothetical prote
c 412 6 6.5 241 2 C64006 probable S-adenosy
c 413 6 6.5 241 2 D43273 heregulin precurs
c 414 6 6.5 241 2 S32359 glial growth facto
c 415 6 6.5 242 2 T16804 hypothetical prote
c 416 6 6.5 244 2 G87545 transcription regu
c 417 6 6.5 244 2 T37686 hypothetical prote
c 418 6 6.5 245 2 T47878 hypothetical prote
c 419 6 6.5 245 2 H88642 protein C54E4.1 [i
c 420 6 6.5 246 2 A72370 regulatory protein
c 421 6 6.5 246 2 T20049 hypothetical prote
c 422 6 6.5 246 2 F95155 ABC transporter, A
c 423 6 6.5 247 2 S03546 hypothetical prote
c 424 6 6.5 247 2 T31811 hypothetical prote
c 425 6 6.5 247 2 T12957 hypothetical prote
c 426 6 6.5 249 2 T21083 hypothetical prote
c 427 6 6.5 249 2 T26482 hypothetical prote
c 428 6 6.5 250 2 E83823 ABC transporter (A
c 429 6 6.5 251 2 A75482 oxidoreductase, sh
c 430 6 6.5 251 2 F86942 conserved hypothet
c 431 6 6.5 251 2 G81923 probable ABC-trans
c 432 6 6.5 251 2 A81180 ABC transporter, A
c 433 6 6.5 252 2 AF1278 indol-3-glycerol p
c 434 6 6.5 252 2 A98022 hypothetical prote
c 435 6 6.5 253 1 R5ZPD4 ribosomal protein
c 436 6 6.5 253 2 H69046 hypothetical prote
c 437 6 6.5 253 2 G75350 conserved hypothet
c 438 6 6.5 254 2 S65465 trypsin-like prote
c 439 6 6.5 254 2 F90107 60S ribosomal prot
c 440 6 6.5 254 2 S50243 ribosomal protein
c 441 6 6.5 255 2 I47092 MHC OVAR-DQ-ALPHA-
c 442 6 6.5 255 2 I47093 hypothetical prote
c 443 6 6.5 255 2 B97861 amidase yedB [limp
c 444 6 6.5 256 2 T44452 ribosomal protein
c 445 6 6.5 257 1 R5RTL8 ribosomal protein
c 446 6 6.5 257 2 JN0923 ribosomal protein
c 447 6 6.5 257 2 S42725 60S ribosomal prot
c 448 6 6.5 258 2 C84559 ribosomal protein
c 449 6 6.5 258 2 T04582 ribosomal protein
c 450 6 6.5 259 2 S30950 gene 2 protein - M
c 451 6 6.5 259 2 T29727 hypothetical prote
c 452 6 6.5 260 1 R5TOL8 ribosomal protein

453 6 6.5 260 2 S22641 ribosomal protein
454 6 6.5 260 2 T18676 hypothetical prote
455 6 6.5 260 2 T45750 ribosomal protein
c 456 6 6.5 260 2 S04647 hypothetical 28.2K
c 457 6 6.5 260 2 E84668 hypothetical prote
458 6 6.5 262 2 C84563 hypothetical prote
459 6 6.5 262 2 T02724 gag protein homolo
c 460 6 6.5 263 2 C56084 interleukin-lbeta
c 461 6 6.5 263 2 AG2280 glutathione S-tran
c 462 6 6.5 264 2 B82619 exodeoxyribonuclea
c 463 6 6.5 264 2 B69937 hypothetical prote
c 464 6 6.5 264 2 T08939 RING zinc finger p
c 465 6 6.5 268 2 AG2594 enoyl-(acyl-carrie
c 466 6 6.5 268 2 A81864 probable NMA1686 l
c 467 6 6.5 269 2 T37073 hypothetical prote
c 468 6 6.5 269 2 T08811 hypothetical prote
c 469 6 6.5 269 2 JC4899 proline rich prote
c 470 6 6.5 270 2 H97376 enoyl-(acyl-carrie
c 471 6 6.5 270 2 AF2159 hypothetical prote
c 472 6 6.5 270 2 S73705 adhesin P1 precurs
c 473 6 6.5 271 2 H84337 spermidine/putresc
c 474 6 6.5 271 2 B60176 hypothetical prote
c 475 6 6.5 273 2 E97293 probable transcrip
c 476 6 6.5 273 2 AC1169 hypothetical prote
c 477 6 6.5 273 2 T44657 protein GP80 limpo
c 478 6 6.5 273 2 T19174 hypothetical prote
c 479 6 6.5 273 2 AB0848 Iron transport pro
c 480 6 6.5 273 2 S20069 ribonucleoprotein
c 481 6 6.5 274 2 F85741 hypothetical prote
c 482 6 6.5 274 2 T15134 hypothetical prote
c 483 6 6.5 274 2 T19466 hypothetical prote
c 484 6 6.5 274 2 E71119 hypothetical prote
c 485 6 6.5 274 2 A12870 metal dependent hy
c 486 6 6.5 274 2 C97647 hypothetical prote
c 487 6 6.5 274 2 T07393 myb-related transc
c 488 6 6.5 275 2 S77388 nitrate transport
c 489 6 6.5 275 2 F82325 conserved hypothet
c 490 6 6.5 276 2 D70953 hypothetical prote
c 491 6 6.5 276 2 S13585 nosY protein precu
c 492 6 6.5 276 2 F95259 conserved hypothet
c 493 6 6.5 276 2 A99525 myelin proteolipid
c 494 6 6.5 277 2 I51270 hypothetical prote
c 495 6 6.5 277 2 AF3024 hypothetical prote
c 496 6 6.5 277 2 C98260 hypothetical prote
c 497 6 6.5 277 2 F97409 hypothetical prote
c 498 6 6.5 278 2 B40825 hypothetical prote
c 499 6 6.5 279 2 AG1307 hypothetical prote
500 6 6.5 279 2 AG1679 hypothetical prote

ALIGNMENTS

RESULT 1

A55406
calgranulin c - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55406
R;Dell'Angelica, E.C.; Schleicher, C.H.; Santome, J.A.
J. Biol. Chem. 269, 28929-28936, 1994
A;Title: Primary structure and binding properties of calgranulin C, a novel S100-like c
A;Reference number: A55406; MUID:95050708; PMID:7961855
A;Accession: A55406
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-91
A;Cross-references: UNIPROT:P80310
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand
F;48-80/Domain: calmodulin repeat homology <EF2>

Alignment Scores: 2.45e-12 Length: 91
Pred. No.:

Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x A55406 (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGAGGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
|||||
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

RESULT 2
A42628
calgranulin B - bovine (fragment)
N/Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor in 2
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997
C:Accession: B22309; A42628
R:Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen, submitted to the Protein Sequence Database, July 1992
A:Reference number: A22309
A:Accession: B22309
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-122 <TAN>
R:Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.
Biochemistry 31, 5898-5905, 1992
A:Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophil
A:Reference number: A42628; MUID:92304974; PMID:1610833
A:Accession: A42628
A:Molecule type: protein
A:Residues: 4-32, F',34-56 <DIA>
C:Complex: heterodimer and higher complexes with calgranulin A
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phospho
F:6-40/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>

Alignment Scores:
Pred. No.: 0.00638 Length: 122
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.96% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x A42628 (1-122)

QY 31 ATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
|||||
Db 11 IleIleAsnIlePheHisGlnTyrSerValArg 21

RESULT 3
JC4712
S-100 calcium-binding protein A12 - human
N/Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; calgranulin protein
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4712; JC4717; JC4891; S56113; S56114
R:Yamamura, T.; Hitomi, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsukada, Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping.
A:Reference number: JC4712; MUID:96192053; PMID:8619860
A:Accession: JC4712
A:Molecule type: mRNA
A:Residues: 1-92 <YAM>
A:Cross-references: UNIPROT:P80511; DDBJ:D83657; NID:g1502284; PIDN:BAA12030.1; PID:g1502284
R:Marti, T.; Ertmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequence

A:Reference number: JC4717; MUID:96192069; PMID:8619876
A:Accession: JC4717
A:Molecule type: protein
A:Residues: 2-92 <MAR>
A:Experimental source: Onchocerca volvulus infecting human tissue
R:Ilg, E.C.; Troxler, H.; Buerigisser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hunz Biochem. Biophys. Res. Commun. 225, 146-150, 1996
A:Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP, A:Reference number: JC4891; MUID:96332419; PMID:8769108
A:Accession: JC4891
A:Molecule type: protein
A:Residues: 2-92 <ILG>
R:Guignard, F.; Mael, J.; Markert, M.
Biochem. J. 309, 395-401, 1995
A:Title: Identification and characterization of a novel human neutrophil protein related
A:Reference number: S56113; MUID:95351965; PMID:7626002
A:Accession: S56113
A:Status: preliminary
A:Molecule type: protein
A:Residues: 'XX',4-14,'X',16-17,'XXXX' <GUI1>
A:Experimental source: isoform 6a
A:Accession: S56114
A:Status: preliminary
A:Molecule type: protein
A:Residues: 2-21 <GUI2>
A:Experimental source: isoform 6b
C:Comment: This protein is released by activated neutrophils in the course of inflammation.
C:Genetics:
A:Gene: GDB:S100A12; p6; MRP6; CGRP; CAAF1
A:Cross-references: GDB:5218374
A:Map position: 1q21-1q21
C:Complex: monomer
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
F:2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAT>
F:6-39/Domain: calmodulin repeat homology <EF1>
F:49-81/Domain: calmodulin repeat homology <EF2>
F:86-90/Region: zinc binding #status predicted

Alignment Scores:
Pred. No.: 0.81 Length: 92
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x JC4712 (1-92)

QY 37 AACATCTTCCACCAGTACTCCGTTCCG 63
|||||
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 4
T12854
hypothetical protein yopT - Bacillus subtilis phage SPBc2
C:Species: Bacillus subtilis phage SPBc2
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T12854; B69918
R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mael, C.; Karamata, D. submitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage
A:Reference number: Z17583
A:Accession: T12854
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-72 <LAZ>
A:Cross-references: UNIPROT:O64103; EMBL:AF020713; NID:g3025478; PID:g3025568; PIDN:AAC
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle:

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.;Authors: Schleith, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69918
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-72 <KUN>
A;Cross-references: GB:Z99114; GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB13995.1; PI
A;Experimental source: strain 168
C;Genetics:
A;Gene: yopT

Alignment Scores:
Pred. No.: 9.19 Length: 72
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T12854 (1-72)
QY 219 TTCTCAAAGCTGACGGCTCCGTC 196
Db 45 PheLeuLysAlaAspGlySerVal 52
RESULT 5
T22414
hypothetical protein F49C12.10 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22414
R;Gardner, A.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19562
A;Accession: T22414
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-275 <WIL>
A;Cross-references: UNIPROT:Q20587; EMBL:Z68227; PIDN:CAA92513.1; GSPDB:GN00022; CESP:F4
A;Experimental source: clone F49C12
C;Genetics:
A;Gene: CESP:F49C12.10
A;Map position: 4
A;Introns: 69/1; 112/2; 152/1; 191/3; 233/3

Alignment Scores:
Pred. No.: 8.35 Length: 275
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T22414 (1-275)
QY 51 GTACTCCGTTCCGGTGGGCATTT 74
Db 174 valLeuArgSerGlyGlyAlaPhe 181
RESULT 6
G71228
hypothetical protein PH0089 - *Pyrococcus horikoshii*
C;Species: *Pyrococcus horikoshii*
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C;Accession: G71228
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: G71228
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-334 <KAW>
A;Cross-references: UNIPROT:O57833; GB:AP000001; NID:g3236128; PIDN:BAA29158.1; PID:g325 A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PH0089

Alignment Scores:
Pred. No.: 8.24 Length: 334
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x G71228 (1-334)
QY 150 ATCTTTGGTGTCTCGGAGGGTTTT 127
Db 272 IlePheGlyValLeuGluGlyPhe 279
RESULT 7
AF2375
hypothetical protein all4558 [imported] - *Nostoc* sp. (strain PCC 7120)
C;Species: *Nostoc* sp. PCC 7120
A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2375
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing *Cyanobacterium Ana*
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2375
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-363 <KUR>
A;Cross-references: UNIPROT:Q8YNK7; GB:BA000019; PIDN:BAF76257.1; PID:g17133694; GSPDB:G A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4558

Alignment Scores:
Pred. No.: 8.19 Length: 363
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AF2375 (1-363)
QY 131 GTTTTGGGAAGTTCCTTTGTGATC 108
Db 156 ValLeuGlySerSerPheValIle 163
RESULT 8
A41258
a-agglutinin core protein AGA1 - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: a-agglutinin attachment protein AGA1; protein N3431; protein YNR044w
C;Species: *Saccharomyces cerevisiae*
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41258; S63375; S17031
R;Roy, A.; Lu, C.F.; Marykwas, D.L.; Lipke, P.N.; Kurjan, J.

Mol. Cell. Biol. 11, 4196-4206, 1991
A;Title: The AGA1 product is involved in cell surface attachment of the Saccharomyces cerevisiae
A;Reference number: A41258; MUID:91304412; PMID:2072914
A;Accession: A41258
A;Molecule type: DNA
A;Residues: 1-725 <ROY>
A;Cross-references: UNIPROT:P32323; GB:M60590; NID:gl70963; PIDN:AAA34382.1; PID:gl70964

R;Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63346
A;Accession: S63375
A;Molecule type: DNA
A;Residues: 1-725 <POH>
A;Cross-references: EMBL:Z71659; NID:gl302551; PIDN:CAA96325.1; PID:e239834; PID:gl302551
A;Experimental source: strain S288C
C;Genetics:

A;Gene: SGD:AGA1
A;Cross-references: SGD:S0005327; MIPS:YNR044w
A;Map position: 14R
C;Keywords: glycoprotein; transmembrane protein
F;8-24/Domain: transmembrane #status predicted <TM1>
F;708-724/Domain: transmembrane #status predicted <TM2>

Alignment Scores:
Pred. No.: 7.79 Length: 725
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x A41258 (1-725)
QY 71 ATTTCGACACCTCAACAAGCGTG 94
Db 634 ILeSerThrProSerThrSerVal 641

RESULT 9
T19351
hypothetical protein C17E4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19351
R;Percy, C.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19113
A;Accession: T19351
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-819 <WIL>
A;Cross-references: UNIPROT:Q93228; EMBL:Z81037; PIDN:CAB02745.1; GSPDB:GN00019; CESP:C17E4
A;Experimental source: clone C17E4
C;Genetics:
A;Gene: CESP:C17E4.2
A;Map position: 1
A;Introns: 151/3; 346/3; 376/2; 446/3; 669/3; 707/3

Alignment Scores:
Pred. No.: 7.73 Length: 819
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T19351 (1-819)
QY 29 GAATCATCAACATCTTCCACCAAGT 52
Db 799 GluSerSerThrSerSerThrSer 806

RESULT 10
B41655

sucrose catabolism protein Scry' - Salmonella thompson plasmid Sac (fragment)
C;Species: Salmonella thompson
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: B41655
R;Cowan, P.J.; Nagesha, H.; Leonard, L.; Howard, J.L.; Pittard, A.J.
J. Bacteriol. 173, 7464-7470, 1991
A;Title: Characterization of the major promoter for the plasmid-encoded sucrose genes
A;Reference number: A41655; MUID:92041657; PMID:1938944
A;Accession: B41655
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-41 <COW>
A;Cross-references: UNIPROT:P24262; GB:M63038; NID:gl54360; PIDN:AAA27218.1; PID:gl54360
C;Genetics:
A;Genome: plasmid

Alignment Scores:
Pred. No.: 107 Length: 41
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x B41655 (1-41)
QY 109 TCAGCTGCTTCAGCTCAGCT 89
Db 16 SerAlaAlaSerAlaHisAla 22

RESULT 11
AH2906
conserved hypothetical protein Atu2689 [imported] - Agrobacterium tumefaciens (strain C58)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AH2906
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, E.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClelland, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2906
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <KUR>
A;Cross-references: UNIPROT:Q8UC09; GB:AE008688; PIDN:AAL43670.1; PID:gl7741195; GSPDB:AB2577
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2689
A;Map position: circular chromosome

Alignment Scores:
Pred. No.: 104 Length: 57
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AH2906 (1-57)
QY 88 AAGCGTGAGCTGAAGCAGCTG 108
Db 33 LysArgGluLeuLysGlnLeu 39

RESULT 12
T03670
reverse transcriptase - rice copia-like retrotransposon Rrt7 (fragment)
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C;Accession: T03670
R;Wang, S.
submitted to the EMBL Data Library, June 1996
A;Description: Copia-like retrotransposons in rice: sequence heterogeneity, species dist
A;Reference number: Z14979
A;Accession: T03670
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-78 <WAN>
A;Cross-references: EMBL:Z75502; NID:e995599; PID:e250631
A;Experimental source: subsp. Japonica, cv. Nongken 58S, leaf
C;Genetics:
A;Mobile element: copia-like retrotransposon Rrt7

Alignment Scores:	102	Length:	78
Pred. No.:	7.00	Matches:	7
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	7.61%	Gaps:	0
DB:	2		

US-09-910-208B-1 (1-276) x T03670 (1-78)

QY 188 GCATCCAGGCTCTTGGAAATATT 168
|||||
Db 47 AlaSerArgSerTrpAsnIle 53

RESULT 13
T03707
reverse transcriptase homolog - rice retrotransposon Tos11 (fragment)
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03707
R;Hirochika, H.; Sugimoto, K.; Otsuki, Y.; Tsugawa, H.; Kanda, M.
Proc. Natl. Acad. Sci. U.S.A. 93, 7783-7788, 1996
A;Title: Retrotransposons of rice involved in mutations induced by tissue culture.
A;Reference number: Z15023; MUID:96353895; PMID:8755553
A;Accession: T03707
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-81 <HIR>
A;Cross-references: UNIPROT:O24195; EMBL:D85869; NID:g1621478; PIDN:BAA12895.1; PID:g162
A;Experimental source: subsp. Japonica, cv. Nipponbare
C;Genetics:
A;Mobile element: retrotransposon Tos11
C;Superfamily: retrovirus-related polypeptide

Alignment Scores:	102	Length:	81
Pred. No.:	7.00	Matches:	7
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	7.61%	Gaps:	0
DB:	2		

US-09-910-208B-1 (1-276) x T03707 (1-81)

QY 188 GCATCCAGGCTCTTGGAAATATT 168
|||||
Db 41 AlaSerArgSerTrpAsnIle 47

RESULT 14
T06548
RNA-directed DNA polymerase (EC 2.7.7.49) - wheat Ty1-copia type retrotransposon (fragme
N;Alternate names: reverse transcriptase
C;Species: Triticum aestivum (common wheat)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06548
R;Hirochika, H.; Hirochika, R.
Jpn. J. Genet. 68, 35-46, 1993
A;Title: Ty1-copia group retrotransposons as ubiquitous components of plant genomes.
A;Reference number: Z15147; MUID:93305354; PMID:8391285

A;Accession: T06548
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-81 <HIR>
A;Cross-references: UNIPROT:Q9ZRL6; EMBL:D12832; NID:g218342; PIDN:BAA02264.1; PID:g2183
C;Genetics:
A;Gene: pol
A;Mobile element: Ty1-copia type retrotransposon
C;Superfamily: retrovirus-related polypeptide
C;Keywords: nucleotidyltransferase

Alignment Scores:	102	Length:	81
Pred. No.:	7.00	Matches:	7
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	7.61%	Gaps:	0
DB:	2		

US-09-910-208B-1 (1-276) x T06548 (1-81)

QY 188 GCATCCAGGCTCTTGGAAATATT 168
|||||
Db 41 AlaSerArgSerTrpAsnIle 47

RESULT 15
T03937
reverse transcriptase - maize Ty1-copia type retrotransposon (fragment)
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03937
R;Hirochika, H.; Hirochika, R.
Jpn. J. Genet. 68, 35-46, 1993
A;Title: Ty1-copia group retrotransposons as ubiquitous components of plant genomes.
A;Reference number: Z15147; MUID:93305354; PMID:8391285
A;Accession: T03937
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-81 <HIR>
A;Cross-references: UNIPROT:Q9ZRL8; EMBL:D12830; NID:g217965; PIDN:BAA02262.1; PID:g217
C;Genetics:
A;Gene: pol
A;Mobile element: Ty1-copia type retrotransposon
C;Superfamily: retrovirus-related polypeptide
C;Keywords: reverse transcriptase

Alignment Scores:	102	Length:	81
Pred. No.:	7.00	Matches:	7
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	7.61%	Gaps:	0
DB:	2		

US-09-910-208B-1 (1-276) x T03937 (1-81)

QY 188 GCATCCAGGCTCTTGGAAATATT 168
|||||
Db 41 AlaSerArgSerTrpAsnIle 47

Search completed: February 23, 2005, 11:45:04
Job time : 38 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:36:26 ; Search time 116 Seconds
(without alignments)
2436.791 Million cell updates/sec

Title: US-09-910-208B-1
Perfect score: 92
Sequence: 1 atgactaagctggaagatca.....acatagatatccacaaagag 276

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3224408

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

-MODEL=frame+n2p,model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/HADDAD-09-910208/runat_23022005_101829_14952/app_query.fasta_1.
-DB=UniProt_03 -QFMT=fastan -SUFFIX=oligo.rup -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208 @CGN 1 1 244 @runat_23022005_101829_14952 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : UniProt 03:*

1: uniprot_sprot:*\n2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	98.9	91	1 S112_BOVIN	P79105 bos taurus
2	64	69.6	70	2 Q9TR16	Q9tr16 bos taurus
3	20	21.7	91	1 S112_PIG	P80310 sus scrofa
4	13	14.1	118	1 S109_RABIT	P50117 oryctolagus
5	11	12.0	122	1 S109_BOVIN	P28783 bos taurus
6	10	10.9	81	1 S112_RABIT	O77791 oryctolagus
7	9	9.8	91	1 S112_HUMAN	P80511 homo sapien
8	9	9.8	568	2 P78947	P78947 schizosacch
9	9	9.8	605	2 Q9HGP1	Q9hgp1 schizosacch
10	8	8.7	72	2 O64103	O64103 bacterioph
11	8	8.7	72	2 O34498	O34498 bacillus su
12	8	8.7	158	2 Q94577	Q94577 heliocidari
13	8	8.7	225	2 Q49597	Q49597 mycobacteri
14	8	8.7	275	2 Q20587	Q20587 caenorhabdi
15	8	8.7	319	2 Q7MSF1	Q7msf1 wolinnella s
16	8	8.7	334	2 O57833	O57833 pyrococcus

90	7	7.6	133	2	Q7SR08	Q7sr08 human immun	163	7	7.6	219	2	Q9BXF1	Q9bxf1 homo sapien
91	7	7.6	133	2	Q7SR09	Q7sr09 human immun	c 164	7	7.6	219	2	Q6QVY9	Q6qvy9 syringa vul
92	7	7.6	133	2	Q7SR10	Q7sr10 human immun	165	7	7.6	220	2	Q6EPS0	Q6eps0 oryza sativ
93	7	7.6	133	2	Q7SR11	Q7sr11 human immun	166	7	7.6	223	2	Q6TVA0	Q6tva0 bovine papu
94	7	7.6	133	2	Q7SR12	Q7sr12 human immun	167	7	7.6	230	2	Q6MKX6	Q6mkx6 bdellovibri
95	7	7.6	133	2	Q7SR13	Q7sr13 human immun	168	7	7.6	230	2	Q8BUL4	Q8bul4 m mus muscu
96	7	7.6	133	2	Q7SR14	Q7sr14 human immun	169	7	7.6	231	2	Q86K19	Q86k19 dictyosteli
97	7	7.6	133	2	Q7SR15	Q7sr15 human immun	170	7	7.6	232	2	Q6BNV5	Q6bnv5 debaryomyce
98	7	7.6	133	2	Q7SR16	Q7sr16 human immun	171	7	7.6	236	2	Q9SJX3	Q9sjx3 arabidopsis
99	7	7.6	133	2	Q7SR19	Q7sr19 human immun	172	7	7.6	239	2	Q9CUK4	Q9cuk4 mus musculu
100	7	7.6	133	2	Q7SR20	Q7sr20 human immun	173	7	7.6	241	2	Q86LY4	Q86ly4 myxine glut
101	7	7.6	133	2	Q7SR21	Q7sr21 human immun	174	7	7.6	243	2	Q8VYM0	Q8vym0 arabidopsis
102	7	7.6	133	2	Q7SR22	Q7sr22 human immun	175	7	7.6	243	2	Q82G51	Q82g51 streptomyce
103	7	7.6	133	2	Q7SR23	Q7sr23 human immun	176	7	7.6	244	2	Q9WVW6	Q9wvw6 pseudomonas
104	7	7.6	133	2	Q7SR24	Q7sr24 human immun	177	7	7.6	245	2	Q9X6H3	Q9x6h3 streptococc
105	7	7.6	133	2	Q7SR25	Q7sr25 human immun	c 178	7	7.6	249	1	CDSA_ECOLI	P06466 e phosphati
106	7	7.6	133	2	Q7SR26	Q7sr26 human immun	179	7	7.6	251	2	Q97CT4	Q97ct4 thermopiasm
107	7	7.6	133	2	Q7SR27	Q7sr27 human immun	c 180	7	7.6	253	1	SOJ_BACHD	Q9k5n0 bacillus ha
108	7	7.6	133	2	Q7SR28	Q7sr28 human immun	181	7	7.6	253	2	Q7XZH6	Q7xzh6 oryza sativ
109	7	7.6	133	2	Q7SR29	Q7sr29 human immun	c 182	7	7.6	255	1	PLSC_NEIGO	Q59601 neisseria g
110	7	7.6	133	2	Q7SR30	Q7sr30 human immun	c 183	7	7.6	255	1	PLSC_NEIMA	Q9ju41 neisseria m
111	7	7.6	135	2	Q9VBV7	Q9vbt9 drosophila	c 184	7	7.6	255	1	PLSC_NEIMB	Q9jz47 neisseria m
c 112	7	7.6	136	2	Q9RBV7	Q9rbv7 pseudomonas	185	7	7.6	256	2	Q9F5M2	Q9f5m2 rhodocycclus
c 113	7	7.6	138	1	GSPI_XANCP	P31738 xanthomonas	c 186	7	7.6	257	2	Q59618	Q59618 neisseria m
c 114	7	7.6	138	2	Q8PGS6	Q8pgs6 xanthomonas	187	7	7.6	261	2	Q97VW6	Q97vw6 sulfolobus
c 115	7	7.6	138	2	Q6APC2	Q6apc2 desulfotale	188	7	7.6	264	2	Q9SPK4	Q9sur4 arabidopsis
c 116	7	7.6	139	2	Q87VZ4	Q87vz4 pseudomonas	189	7	7.6	268	2	Q95PK4	Q95pk4 tribolium c
c 117	7	7.6	140	2	Q86Q31	Q86q31 hydra atten	190	7	7.6	269	2	Q6ATR6	Q6atr6 oryza sativ
c 118	7	7.6	140	2	Q9CXQ6	Q9cxq6 mus musculu	191	7	7.6	271	1	OLG1_HUMAN	Q8tak6 homo sapien
c 119	7	7.6	141	2	Q58631	Q58631 pyrococcus	192	7	7.6	271	2	Q8NTB2	Q8ntb2 corynebacte
c 120	7	7.6	145	2	Q8VU96	Q8vu96 lactobacill	193	7	7.6	271	2	Q88T01	Q88t01 lactobacill
c 121	7	7.6	149	2	Q6VAQ6	Q6vaq6 onchidella	194	7	7.6	272	2	Q64594	Q64594 arabidopsis
c 122	7	7.6	149	2	Q7F1U4	Q7flu4 oryza sativ	195	7	7.6	276	2	Q6PWY0	Q6pwy0 rattus norv
c 123	7	7.6	151	2	Q8BK94	Q8bk94 mus musculu	c 196	7	7.6	277	2	Q8R0B6	Q8r0b6 mus musculu
c 124	7	7.6	152	2	Q7QCA9	Q7qca9 anopheles g	c 197	7	7.6	277	2	Q8BG34	Q8bg34 m mus muscu
c 125	7	7.6	156	2	Q7PWZ0	Q7pwz0 anopheles g	c 198	7	7.6	277	2	Q8BP58	Q8bp58 mus musculu
c 126	7	7.6	158	2	Q6J654	Q6j654 dendrolimus	c 199	7	7.6	281	2	Q9P632	Q9p632 neurospora
c 127	7	7.6	163	2	Q88167	Q88167 agrobacteri	200	7	7.6	281	2	Q8XU00	Q8xuu0 ralstonia s
c 128	7	7.6	169	2	Q8VAW8	Q8vaw8 white spot	c 201	7	7.6	283	2	Q961J0	Q96ij0 homo sapien
c 129	7	7.6	170	2	Q9XSE5	Q9xse5 sus scrofa	c 202	7	7.6	284	2	Q7QKS7	Q7qks7 giardia lam
c 130	7	7.6	171	2	Q75CM7	Q75cm7 ashbya goss	c 203	7	7.6	285	2	Q7XKP6	Q7xkp6 oryza sativ
c 131	7	7.6	185	2	Q9B0V5	Q9b0v5 locustacaru	c 204	7	7.6	285	2	Q74KZ3	Q74kz3 lactobacill
c 132	7	7.6	185	2	Q9B9T8	Q9b9t8 locustacaru	c 205	7	7.6	285	2	Q60501	Q60501 cricetus
c 133	7	7.6	185	2	Q9B9T9	Q9b9t9 locustacaru	206	7	7.6	291	2	Q8V7H6	Q8v7h6 tt virus. o
c 134	7	7.6	185	2	Q9B9U0	Q9b9u0 locustacaru	207	7	7.6	293	2	P96725	P96725 bacillus su
c 135	7	7.6	185	2	Q9B9U1	Q9b9u1 locustacaru	208	7	7.6	301	2	Q9W417	Q9w417 drosophila
c 136	7	7.6	185	2	Q9B9U2	Q9b9u2 locustacaru	c 209	7	7.6	303	2	Q64RT8	Q64rt8 bacteroides
c 137	7	7.6	188	2	Q6CT23	Q6ct23 kluyveromyc	c 210	7	7.6	303	2	Q7ZXR9	Q7zxr9 xenopus lae
c 138	7	7.6	199	2	Q8Y0T8	Q8y0t8 ralstonia s	c 211	7	7.6	305	2	Q65KP7	Q65kp7 bacillus li
c 139	7	7.6	202	2	Q8IXQ8	Q8ixq8 homo sapien	c 212	7	7.6	306	2	Q8NXP4	Q8nxp4 staphylococ
c 140	7	7.6	202	2	Q65136	Q65i36 syringa vul	213	7	7.6	306	2	Q7A2V4	Q7a2v4 staphylococ
c 141	7	7.6	204	2	Q05652	Q05652 bacillus ce	214	7	7.6	306	2	Q7A6W0	Q7a6w0 staphylococ
c 142	7	7.6	204	2	Q72Y51	Q72y51 bacillus ce	215	7	7.6	306	2	Q8CTI6	Q8cti6 staphylococ
c 143	7	7.6	204	2	Q815V1	Q815v1 bacillus ce	216	7	7.6	306	2	Q9KWK1	Q9kwk1 staphylococ
c 144	7	7.6	204	2	Q6HBM6	Q6hbm6 bacillus th	217	7	7.6	306	2	Q6GBD1	Q6gbd1 staphylococ
c 145	7	7.6	204	2	Q7TS73	Q7ts73 mus musculu	218	7	7.6	306	2	Q6GIU3	Q6giu3 staphylococ
c 146	7	7.6	208	2	Q18579	Q18579 caenorhabdi	c 219	7	7.6	308	2	Q8WUI3	Q8wui3 homo sapien
c 147	7	7.6	208	2	Q8MU76	Q8mu76 anopheles g	c 220	7	7.6	308	2	Q619Z2	Q6i9z2 homo sapien
c 148	7	7.6	208	2	Q8T5H7	Q8t5h7 anopheles g	c 221	7	7.6	308	2	Q9H5P9	Q9h5p9 homo sapien
c 149	7	7.6	208	2	Q7PKT5	Q7pkt5 anopheles g	222	7	7.6	308	2	Q8VGA4	Q8vga4 mus musculu
150	7	7.6	210	1	INSR_MACMU	Q28516 macaca mula	c 223	7	7.6	309	1	CEO1_LACLA	Q9cg73 lactococcus
151	7	7.6	210	2	Q6PS86	Q6ps86 streptococc	c 224	7	7.6	309	2	Q61F41	Q6if41 homo sapien
152	7	7.6	211	2	Q95NI6	Q95ni6 tribolium c	c 225	7	7.6	310	2	Q8NGT8	Q8ngt8 homo sapien
153	7	7.6	211	2	Q95UA8	Q95ua8 tribolium c	226	7	7.6	311	2	Q6BUW0	Q6buw0 debaryomyce
154	7	7.6	212	1	KAD_STRR6	Q8drd4 streptococc	227	7	7.6	312	2	Q9BK04	Q9bk04 tribolium c
155	7	7.6	212	2	Q9S4J5	Q9s4j5 streptococc	c 228	7	7.6	313	1	CEO2_LACLA	Q9nhb7 tribolium c
156	7	7.6	213	2	Q7XPT0	Q7xpt0 oryza sativ	229	7	7.6	313	2	O28600	P15244 lactococcus
157	7	7.6	214	2	Q9Q8T1	Q9q8t1 rabbit fibr	230	7	7.6	314	2	Q6NX20	Q6nx20 xenopus tro
c 158	7	7.6	215	2	Q6CIH4	Q6cih4 kluyveromyc	c 231	7	7.6	314	2	Q8VGA2	Q8vga2 mus musculu
c 159	7	7.6	215	2	Q6H5V7	Q6h5v7 oryza sativ	232	7	7.6	315	2	Q7TR60	Q7tr60 mus musculu
160	7	7.6	217	1	GT27_FASHE	P31670 fasciola he	233	7	7.6	315	2	Q9KM43	Q9km43 vibrio chol
161	7	7.6	218	2	Q9XYL9	Q9xyl9 fasciola gi	234	7	7.6	318	2	Q75WE6	Q75we6 penicillium
162	7	7.6	219	2	Q9P3F8	Q9p3f8 neurospora	235	7	7.6	320	2		

236	7	7.6	320	2	Q6SL44	Q6sl44 armillifer	c	309	7	7.6	421	2	Q6W2X0	Q6w2x0 human immun
c 237	7	7.6	323	2	Q36000	Q36000 trichomitus		310	7	7.6	422	2	Q65CX1	Q65cx1 bacillus li
c 238	7	7.6	325	2	Q8W580	Q8w580 arabidopsis		311	7	7.6	424	2	Q61444	Q61444 drosophila
c 239	7	7.6	327	1	NIT1_HUMAN	Q86x76 homo sapien		312	7	7.6	424	2	Q7KPK6	Q7kpk6 drosophila
240	7	7.6	328	2	Q88Z82	Q88z82 lactobacilli		313	7	7.6	424	2	Q7KPK5	Q7kpk5 drosophila
241	7	7.6	330	2	Q6BXP9	Q6bxp9 debaryomyce		314	7	7.6	426	2	Q9NF73	Q9nfh3 drosophila
c 242	7	7.6	330	2	Q92XE3	Q92xe3 rhizobium m	c	315	7	7.6	426	2	Q9SD13	Q9sd13 arabidopsis
243	7	7.6	332	2	Q02796	Q02796 saccharomyc		316	7	7.6	430	2	Q8LSR8	Q8lser8 oryza sativ
244	7	7.6	332	2	Q6Q518	Q6q518 saccharomyc		317	7	7.6	434	2	Q9C979	Q9c979 arabidopsis
245	7	7.6	334	2	Q9ABN8	Q9abn8 caulobacter		318	7	7.6	436	2	Q18714	Q18714 leishmania
c 246	7	7.6	338	2	Q6P4C0	Q6p4c0 homo sapien	c	319	7	7.6	438	2	Q9HUD9	Q9hud9 pseudomonas
247	7	7.6	338	2	Q44936	Q44936 strongyloce		320	7	7.6	439	2	Q86MJ3	Q86mj3 caenorhabdi
248	7	7.6	338	2	Q95Y19	Q95y19 caenorhabdi		321	7	7.6	440	2	Q9P566	Q9p566 neurospora
249	7	7.6	342	2	Q06148	Q06148 saccharomyc		322	7	7.6	441	2	Q6M4A0	Q6m4a0 corynebacte
c 250	7	7.6	344	2	Q9LG29	Q9lg29 arabidopsis		323	7	7.6	441	2	Q8NPF4	Q8np94 corynebacte
251	7	7.6	344	2	Q9RWF7	Q9rwf7 deinococcus	c	324	7	7.6	448	2	Q7R090	Q7r090 giardia lam
252	7	7.6	345	2	Q8WZ17	Q8wzi17 penicillium		325	7	7.6	456	2	Q9LQA0	Q9lqa0 arabidopsis
253	7	7.6	347	1	DTX3_HUMAN	Q8n9i9 homo sapien		326	7	7.6	456	2	Q9XCK8	Q9xck8 streptococc
254	7	7.6	347	1	DTX3_MOUSE	Q80v91 mus musculu	c	327	7	7.6	462	2	Q7XVS1	Q7xvs1 oryza sativ
255	7	7.6	347	2	Q8JFW8	Q8jfw8 brachydanio		328	7	7.6	463	2	Q7S427	Q7s427 neurospora
256	7	7.6	349	2	Q9AR58	Q9ar58 solanum tub		329	7	7.6	463	2	Q6UU50	Q6uu50 oryza sativ
257	7	7.6	349	2	Q9ZP53	Q9zp53 solanum tub		330	7	7.6	463	2	Q803Y5	Q803y5 brachydanio
258	7	7.6	349	2	Q8FSE8	Q8fse8 corynebacte		331	7	7.6	464	2	Q8MZR6	Q8mzr6 ctenocephal
259	7	7.6	351	2	Q88536	Q88536 mus musculu		332	7	7.6	464	2	Q86MJ4	Q86mj4 caenorhabdi
260	7	7.6	353	2	Q7SP02	Q7sf02 neurospora		333	7	7.6	465	2	Q9HFT4	Q9hft4 pleurotus s
c 261	7	7.6	353	2	Q98BM1	Q98bm1 rhizobium l		334	7	7.6	466	2	Q6BHI1	Q6bhi1 debaryomyce
262	7	7.6	370	2	Q74012	Q740i2 mycobacteri		335	7	7.6	469	2	Q8U254	Q8u254 pyrococcus
c 263	7	7.6	363	2	Q7T2F4	Q7t2f4 brachydanio		336	7	7.6	469	2	Q8MQS2	Q8mqse2 drosophila
c 264	7	7.6	366	2	Q8VQW5	Q8vqw5 azotobacter		337	7	7.6	469	2	Q91QP5	Q91qp5 melon yello
c 265	7	7.6	368	2	Q6AL75	Q6al75 desulfotale		338	7	7.6	469	2	Q9WBS2	Q9wbs2 physalis se
c 266	7	7.6	368	2	Q8VCV4	Q8vcv4 mus musculu	c	339	7	7.6	474	2	Q28424	Q28424 archaeoglob
267	7	7.6	369	2	Q7S4Z9	Q7s4z9 neurospora		340	7	7.6	475	1	SIM1_YEAST	P40472 saccharomyc
268	7	7.6	369	2	Q8XXD5	Q8xxd5 ralstonia s	c	341	7	7.6	475	2	Q7CUZ5	Q7cu25 agrobacteri
c 269	7	7.6	370	2	Q6Z0L8	Q6z0l8 oryza sativ	c	342	7	7.6	476	2	Q651C2	Q651c2 oryza sativ
270	7	7.6	373	1	YLU2_PICAN	P34735 pichia angu	c	343	7	7.6	477	2	Q6MP47	Q6mp47 bdellovibri
271	7	7.6	376	1	MID2_YEAST	P36027 saccharomyc		344	7	7.6	478	2	Q6CFN8	Q6cfn8 yarrowia li
272	7	7.6	377	2	Q8P7Z1	Q8p7z1 xanthomonas		345	7	7.6	481	2	Q989D0	Q989d0 rhizobium l
273	7	7.6	378	2	Q9W1Z4	Q9wlz4 drosophila	c	346	7	7.6	482	2	Q29120	Q29120 archaeoglob
274	7	7.6	379	2	Q6MYT6	Q6myt6 aspergillus	c	347	7	7.6	488	2	Q18545	Q18545 caenorhabdi
c 275	7	7.6	379	2	Q8YVJ5	Q8ymj5 anabaena sp		348	7	7.6	490	2	Q7NQA3	Q7nqa3 chromobacte
c 276	7	7.6	380	2	Q15885	Q15885 homo sapien	c	349	7	7.6	495	2	Q6IMF0	Q6imf0 mus musculu
c 277	7	7.6	381	2	Q67LH1	Q67lh1 symbiobacte	c	350	7	7.6	496	2	Q6C7M6	Q6c7m6 yarrowia li
c 278	7	7.6	384	2	Q91619	Q9i6i9 pseudomonas	c	351	7	7.6	496	2	Q88VA6	Q88va6 lactobacilli
279	7	7.6	387	2	Q8SYN0	Q8syn0 drosophila		352	7	7.6	499	2	Q8BX37	Q8bx37 m mus muscu
280	7	7.6	387	2	Q9ZJN7	Q9zjn7 helicobacte		353	7	7.6	499	2	Q95ZK5	Q95zk5 caenorhabdi
c 281	7	7.6	388	2	Q73GJ2	Q73gj2 wolbachia p	c	354	7	7.6	501	2	Q7XMT3	Q7xmt3 oryza sativ
c 282	7	7.6	389	2	Q84SE0	Q84se0 oryza sativ		355	7	7.6	503	1	PUR1_PASMU	Q916b8 pasteurella
283	7	7.6	390	2	Q6CX47	Q6cx47 yarrowia li		356	7	7.6	504	2	Q9HR41	Q9hr41 halobacteri
284	7	7.6	393	2	Q9RX12	Q9rx12 deinococcus	c	357	7	7.6	505	1	SCRY_SALTY	P22340 salmonella
c 285	7	7.6	394	2	Q67317	Q67317 aquifex ao	c	358	7	7.6	505	2	Q6RZ11	Q6rz11 escherichia
c 286	7	7.6	397	2	Q6C8P0	Q6c8p0 yarrowia li		359	7	7.6	505	2	Q8PQ85	Q8pq85 xanthomonas
c 287	7	7.6	399	2	Q9HJE6	Q9hje6 thermoplasm		360	7	7.6	506	2	Q9CA74	Q9ca74 arabidopsis
288	7	7.6	399	2	Q9LPK4	Q9lpk4 arabidopsis		361	7	7.6	510	2	Q6SCJ8	Q6scj8 aspergillus
289	7	7.6	401	2	Q6AU99	Q6au99 oryza sativ	c	362	7	7.6	512	2	Q95SN6	Q95sn6 drosophila
c 290	7	7.6	402	1	OXAL_YEAST	P39952 saccharomyc	c	363	7	7.6	512	2	Q7WUH1	Q7wuh1 escherichia
291	7	7.6	405	1	HMX_STRPU	Q26656 strongyloce	c	364	7	7.6	513	2	Q8VYV9	Q8vyv9 arabidopsis
292	7	7.6	407	2	Q7NA66	Q7ma66 wolinnella s		365	7	7.6	514	2	Q73QS1	Q73gs1 treponema d
293	7	7.6	407	2	Q9RI96	Q9ri96 streptomyce		366	7	7.6	518	2	Q97DP7	Q97dp7 clostridium
c 294	7	7.6	409	2	Q7BT32	Q7bt32 streptomyce	c	367	7	7.6	519	2	Q755V0	Q755v0 ashbya goss
295	7	7.6	410	2	P72472	P72472 streptomyce		368	7	7.6	519	2	Q8W4X8	Q8w4x8 nicotiana a
c 296	7	7.6	410	2	Q92EP3	Q92ep3 listeria in		369	7	7.6	524	2	Q86MJ5	Q86mj5 caenorhabdi
297	7	7.6	410	2	Q89NX5	Q89nx5 bradyrhizob	c	370	7	7.6	525	2	Q7Z3A6	Q7z3a6 homo sapien
c 298	7	7.6	411	2	Q63MR8	Q63mr8 burkholderi		371	7	7.6	528	1	NU59_YEAST	Q05166 saccharomyc
c 299	7	7.6	414	2	Q6W2W2	Q6w2w2 human immun		372	7	7.6	528	2	Q6B1V8	Q6b1v8 saccharomyc
300	7	7.6	417	2	Q7PS00	Q7ps00 anopheles g		373	7	7.6	528	2	Q72IH1	Q72ih1 thermus the
301	7	7.6	421	2	Q07009	Q07009 bacillus su		374	7	7.6	529	1	LAC1_PLEOS	Q12729 pleurotus o
c 302	7	7.6	421	2	Q6W2V9	Q6w2v9 human immun		375	7	7.6	529	2	Q8WZJ4	Q8wzj4 penicillium
c 303	7	7.6	421	2	Q6W2W4	Q6w2w4 human immun		376	7	7.6	529	2	Q68HC2	Q68hc2 penicillium
c 304	7	7.6	421	2	Q6W2W5	Q6w2w5 human immun		377	7	7.6	529	2	Q6RYA4	Q6rya4 pleurotus o
c 305	7	7.6	421	2	Q6W2W6	Q6w2w6 human immun		378	7	7.6	530	2	Q8RW07	Q8rw07 solanum tub
c 306	7	7.6	421	2	Q6W2W7	Q6w2w7 human immun		379	7	7.6	531	2	Q6A1A1	Q6a1a1 pleurotus s
c 307	7	7.6	421	2	Q6W2W8	Q6w2w8 human immun	c	380	7	7.6	532	2	Q8WZL0	Q8wzl0 neurospora
c 308	7	7.6	421	2	Q6W2W9	Q6w2w9 human immun		381	7	7.6	532	2	Q7Z8S3	Q7z8s3 pleurotus s

RL J. Cell Sci: 109:805-815(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=99325504; PubMed=10399917; DOI=10.1016/S0092-8674(00)80801-6;

RA Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C.,

RA Kambham N., Bierhaus A., Nawroth P., Neurath M.F., Slattey T.,

RA Beach D., McClary J., Nagashima M., Morser J., Stern D., Schmidt A.M.,

RT "RAGE mediates a novel proinflammatory axis: a central cell surface

RT receptor for S100/calgranulin polypeptides.";

RL Cell 97:889-901(1999).

CC -!- SIMILARITY: Belongs to the S-100 family.

CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.

CC -----

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DR EMBL; D49548; BAA08496.1; --.

DR EMBL; AF011757; AAB65423.1; --.

DR HSSP; P80511; 1GQM.

DR InterPro; IPR001751; CaBP_S100.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF_Hand_like.

DR Pfam; PF00036; ehand; 1.

DR Pfam; PF01023; S_100; 1.

DR ProDom; PD003407; CaBP_S100; 1.

DR PROSITE; PS00018; EF_HAND; 1.

DR PROSITE; PS00303; S100_CaBP; 1.

KW Calcium-binding; Metal-binding; Zinc.

FT INIT MET 0 By similarity.

FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).

FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).

SQ SEQUENCE 91 AA; 10554 MW; 66PBC3C1B0354482 CRC64;

Alignment Scores:

Pred. No.:	4.77e-84	Length:	91
Score:	91.00	Matches:	91
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.91%	Indels:	0
DB:	1	Gaps:	0

US-09-910-208B-1 (1-276) x S112_BOVIN (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGAGGGAATCATCAATCTTCCACCAGTACTCCGTTCCG 63

Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 GTGGGCGATTTGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACCTT 123

Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCCAAACCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAAGACCTG 183

Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATCGCGATAAAGACGGAGCCCTCAGCTTTTGAGGAATTCGTAGTCTCTGTTCCAGGGTG 243

Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAAAACAGCCACATAGATATATCCACAAGAG 276

Db 81 LeuLysThrAlaHisIleAspIleHisLysGlu 91

RESULT 2

Q9TR16

ID Q9TR16 PRELIMINARY; PRT; 70 AA.

AC Q9TR16;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE CORNEA-associated antigen, CO-AG=CALGRANULIN C homolog.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=96181454; PubMed=8603881;

RA Liu S.H., Gottsch J.D.;

RT "Amino acid sequence of an immunogenic corneal stromal protein.";

RL Invest. Ophthalmol. Vis. Sci. 37:944-948(1996).

CC -!- SIMILARITY: Belongs to the S-100 family.

DR HSSP; P80511; 1E8A.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR InterPro; IPR001751; CaBP_S100.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF_Hand_like.

DR Pfam; PF01023; S_100; 1.

DR ProDom; PD003407; CaBP_S100; 1.

SQ SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;

Alignment Scores:

Pred. No.:	2.39e-56	Length:	70
Score:	64.00	Matches:	64
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.57%	Indels:	0
DB:	2	Gaps:	0

US-09-910-208B-1 (1-276) x Q9TR16 (1-70)

QY 4 ACTAAGCTGGAAGATCACCTGAGGGAATCATCAATCTTCCACCAGTACTCCGTTCCG 63

Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 GTGGGCGATTTGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACCTT 123

Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 CCCAAACCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAAGACCTG 183

Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATCGCGATAAA 195

Db 61 AspAlaAspLys 64

RESULT 3

S112_PIG

ID S112_PIG STANDARD; PRT; 91 AA.

AC P80310;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Calgranulin C (CAGC).

GN Name=S100A12;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE.

RX TISSUE=Granulocyte;

RX MEDLINE=95050708; PubMed=7961855;

RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;

RT "Primary structure and binding properties of calgranulin C, a novel

RT S100-like calcium-binding protein from pig granulocytes.";

RL J. Biol. Chem. 269:28929-28936(1994).

CC -!- TISSUE SPECIFICITY: Found essentially in granulocytes with small

RL Biochemistry 31:5898-5905(1992).
CC -!- SUBUNIT: Disulfide linked heterodimer of a 7/11 kDa and a 22/23
CC kDa subunits.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; loosely associated to the
CC cytoskeleton.
CC -!- TISSUE SPECIFICITY: Found essentially in phagocytic cells.
CC -!- PTM: Phosphorylated by protein kinase C.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
DR HSSP; P06702; IIRJ.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; PARTIAL.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Direct protein sequencing; Phosphorylation.
FT NON_TER 1
FT CA_BIND 19 32 EF-hand 1; low affinity (Potential).
FT CA_BIND 63 74 EF-hand 2; high affinity (Potential).
SQ SEQUENCE 122 AA; 13673 MW; F3CA8C48806BECCD CRC64;

Alignment Scores:
Pred. No.: 0.0498 Length: 122
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.96% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S109_BOVIN (1-122)

QY 31 ATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 11 IleIleAsnIlePheHisGlnTyrSerValArg 21

RESULT 6
S112 RABBIT
ID S112_RABBIT STANDARD; PRT; 81 AA.
AC O77791;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC) (Fragment).
GN Name=S100A12;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=New Zealand white; TISSUE=Neutrophils;
RX MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
RA Yang Z., DeVeer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
RA Underwood J.R., Robinson H.C.;
RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
RT calgranulin C when incubated with inorganic [35S]sulfate."
RL J. Biol. Chem. 271:19802-19809(1996).
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
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CC -----
DR EMBL; AF091848; AAC61770.1; --
DR HSSP; P80511; 1E8A.

DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Direct protein sequencing.
FT NON_TER 1
FT CA_BIND 8 21 EF-hand 1; low affinity (By similarity).
FT CA_BIND 51 62 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 81 AA; 9401 MW; 95E67A209180CB66 CRC64;

Alignment Scores:
Pred. No.: 0.554 Length: 81
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.87% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_RABIT (1-81)

QY 34 ATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 IleAsnIlePheHisGlnTyrSerValArg 10

RESULT 7
S112 HUMAN
ID S112_HUMAN STANDARD; PRT; 91 AA.
AC P80511; P83219;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Calgranulin C (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding
DE protein in amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].
GN Name=S100A12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1;
RA Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;
RT "Characterization of the human S100A12 (calgranulin C, p6, CAAF1,
RT CGRP) gene, a new member of the S100 gene cluster on chromosome
RT 1q21."
RL Cell Calcium 20:459-464(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96192053; PubMed=8619860; DOI=10.1006/bbrc.1996.0600;
RA Yamamura T., Hitomi J., Nagaesaki K., Suzuki M., Takahashi E.,
RA Saito S., Tsukada T., Yamaguchi K.;
RT "Human CAAF1 gene -- molecular cloning, gene structure, and chromosome
RT mapping."
RL Biochem. Biophys. Res. Commun. 221:356-360(1996).
RN [3]
RP SEQUENCE.
RX MEDLINE=96192069; PubMed=8619876; DOI=10.1006/bbrc.1996.0616;
RA Marti T., Erttmann K.D., Gallin M.Y.;
RT "Host-parasite interaction in human onchocerciasis: identification and
RT sequence analysis of a novel human calgranulin."
RL Biochem. Biophys. Res. Commun. 221:454-458(1996).
RN [4]
RP SEQUENCE.
RC TISSUE=Neutrophils;
RX MEDLINE=96332419; PubMed=8769108; DOI=10.1006/bbrc.1996.1144;
RA Ilg E.C., Troxler H., Buergisser D.M., Kuster T., Markert M.,
RA Guignard F., Hunziker P., Birchler N., Heizmann C.W.;
RT "Amino acid sequence determination of human S100A12 (P6, calgranulin
RT C, CGRP, CAAF1) by tandem mass spectrometry.";

RL Biochem. Biophys. Res. Commun. 225:146-150(1996).

RN [5] SEQUENCE OF 1-20.

RP MEDLINE=95351965; PubMed=7626002;

RA Guignard F., Maue J., Markert M.;

RX "Identification and characterization of a novel human neutrophil

RT protein related to the S100 family.";

RL Biochem. J. 309:395-401(1995).

RN [6] SEQUENCE OF 77-91, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY.

RP TISSUE=Nasal mucus;

RX MEDLINE=21413725; PubMed=11522286; DOI=10.1016/S0014-5793(01)02731-4;

RA Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;

RX "Calcitermin, a novel antimicrobial peptide isolated from human airway

RT secretions.";

RL FEBS Lett. 504:5-10(2001).

RN [7] X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).

RP MEDLINE=21065388; PubMed=11134923; DOI=10.1107/S090744490001458X;

RX Moroz O.V., Antson A.A., Murshudov G.N., Maitland N.J., Dodson G.G.,

RA Wilson K.S., Skibshoj I., Lukanidin E.M., Bronstein I.B.;

RX "The three-dimensional structure of human S100A12.";

RL Acta Crystallogr. D 57:20-29(2001).

CC -!- FUNCTION: Calcitermin possesses antifungal activity against

CC C. albicans and is also active against E.coli and P.aeruginosa but

CC not L.mohocytogenes and S.aureus.

CC -!- SUBUNIT: Homodimer.

CC -!- TISSUE SPECIFICITY: Monocytes and lymphocytes.

CC -!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=1-91;

CC NOTE=Ref.6.

CC -!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=77-91;

CC NOTE=Ref.6.

CC -!- SIMILARITY: Belongs to the S-100 family.

CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.

CC -----

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CC -----

DR EMBL; X97859; CAA66453.1; -.

DR EMBL; X98288; CAA66934.1; -.

DR EMBL; X98289; CAA66934.1; JOINED.

DR EMBL; X98290; CAA66934.1; JOINED.

DR EMBL; X98289; CAB94792.1; -.

DR EMBL; X98290; CAB94792.1; JOINED.

DR EMBL; D49549; BAA08497.1; -.

DR EMBL; D83664; BAA12036.1; -.

DR EMBL; D83657; BAA12030.1; -.

DR PIR; JC4712; JC4712.

DR PDB; 1E8A; X-ray; A/B=1-91.

DR PDB; 1GQM; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-91.

DR PDB; 1ODB; X-ray; A/B/C/D/E/F=1-91.

DR Genew; HGNC:10489; S100A12.

DR MIM; 603112; -.

DR GO; GO:0005829; C:cytosol; TAS.

DR GO; GO:0005626; C:insoluble fraction; TAS.

DR GO; GO:0005509; F:calcium ion binding; TAS.

DR GO; GO:0006954; P:inflammatory response; TAS.

DR InterPro; IPR001751; CaBP_S100.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF_Hand_like.

DR Pfam; PF00036; ehand; 1.

DR Pfam; PF01023; S_100; 1.

DR ProDom; PD003407; CaBP_S100; 1.

DR PROSITE; PS00018; EF_HAND; FALSE_NEG.

DR PROSITE; PS00303; S100_CABP; 1.

KW 3D-structure; Antibiotic; Calcium-binding; Direct protein sequencing;

KW Fungicide; Metal-binding; Zinc.

FT INIT MET 0 0

FT PEPTIDE 77 91 Calcitermin.

FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).

FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).

FT HELIX 2 18

FT TURN 19 19

FT TURN 24 25

FT STRAND 26 27

FT HELIX 29 39

FT TURN 41 43

FT TURN 45 48

FT HELIX 50 60

FT TURN 62 63

FT STRAND 68 69

FT HELIX 70 85

SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;

Alignment Scores:

Pred. No.: 5.79 Length: 91

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 9.78% Indels: 0

DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_HUMAN (1-91)

Qy 37 AACATCTTCCACCAGTACTCCGTTCCG 63

Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 8

P78947 ID P78947 PRELIMINARY; PRT; 568 AA.

AC P78947;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Similer to pir: S52731.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972h-;

RA Kohnosu A., Niwa O., Yano M., Saitoh S., Katayama T., Nagao K.,

RA Yanagida M.;

RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; D83993; BAA12197.1; -.

SQ SEQUENCE 568 AA; 64255 MW; CBF7BD60B8F0DFA6 CRC64;

Alignment Scores:

Pred. No.: 4.7 Length: 568

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 9.78% Indels: 0

DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x P78947 (1-568)

Qy 200 CCGTCTTTATCGGCATCCAGGTCTTGG 174

Db 154 ProSerLeuSerAlaSerArgSerTrp 162

RESULT 9

Q9HGP1 ID Q9HGP1 PRELIMINARY; PRT; 605 AA.

AC Q9HGP1;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE SPBC29B5.04c protein.
GN Name=SPBC29B5.04c;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
RA Gabel C., Fuchs M., Dusterhoft A., Fritzc C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Calibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
DR EMBL; AL391603; CAC05513.1; -.
DR GeneDB_SPombe; SPBC29B5.04c; -.
SQ SEQUENCE 605 AA; 68508 MW; 24558A5C0357448F CRC64;

Alignment Scores:
Pred. No.: 4.67 Length: 605
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q9HGP1 (1-605)

QY 200 CCGTCCTTATCGGCATCCAGGCTCTGG 174
|||||
Db 154 ProSerLeuSerAlaSerArgSerTrp 162

RESULT 10

O64103
ID O64103 PRELIMINARY; PRT; 72 AA.
AC O64103;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein yopT.

GN Name=yopT;
OS Bacteriophage SPBc2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=66797;
RN [1]
RP SEQUENCE FROM N.A.

RA Lazarevic V., Dusterhoeft A., Soldo B., Hilbert H., Mauel C.,
RA Karamata D.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020713; AAC13063.1; -.

DR PIR; T12854; T12854.
KW Hypothetical protein.
SQ SEQUENCE 72 AA; 8078 MW; EF0EFA5D3DE275A4 CRC64;

Alignment Scores:
Pred. No.: 63.1 Length: 72
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x O64103 (1-72)

QY 219 TTCCTCAAAGCTGACGGCTCCGTC 196
|||||
Db 45 PheLeuLysAlaAspGlySerVal 52

RESULT 11

O34498
ID O34498 PRELIMINARY; PRT; 72 AA.
AC O34498;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE YopT protein.
GN Name=yopT; OrderedLocusNames=BSU20770;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=168;

RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
RL Nature 390:249-256(1997).
DR EMBL; 299114; CAB13969.1; -.

KW Complete proteome.

SQ SEQUENCE 72 AA; 8078 MW; EF0EFA5D3DE275A4 CRC64;

Alignment Scores:

Pred. No.: 63.1 Length: 72
Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q34498 (1-72)

Qy 219 TTCTCAAAGCTGACGGCTCGTC 196
|||||
Db 45 PheLeuLysAlaAspGlySerVal 52

RESULT 12

Q94577

ID Q94577 PRELIMINARY; PRT; 158 AA.

AC Q94577;

DT 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE HEHBOX7 (Fragment).

GN Name=HeHbox7;

OS Helicoidaris erythrogramma (Sea urchin).

OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

OC Echinoidae; Euechinoidae; Echinacea; Echinoida; Echinometridae;

OC Helicoidaris.

OX NCBI_TaxID=7634;

RN [1]

RP SEQUENCE FROM N.A.

RA Popodi E., Andrews M.E., Kissinger J.C., Raff R.A.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

DR EMBL; U31564; AAB09407.1; -.

DR HSSP; P09631; 1PUF.

DR TRANSFAC; T03769; -.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR001356; Homeobox.

DR InterPro; IPR009057; Homeodomain like.

DR InterPro; IPR000047; HTH_lambrepresr.

DR Pfam; PF00046; Homeobox; 1.

DR PRINTS; PR00024; HOMEBOX.

DR PRINTS; PR00031; HTHREPRESSR.

DR SMART; SM00389; HOX; 1.

DR PROSITE; PS00027; HOMEBOX_1; 1.

DR PROSITE; PS50071; HOMEBOX_2; 1.

KW DNA-binding; Homeobox; Nuclear protein.

FT NON TER 1

SQ SEQUENCE 158 AA; 18102 MW; B92185FEAA4CB148 CRC64;

Alignment Scores:

Pred. No.: 57.7 Length: 158

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 8.70% Indels: 0

DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q94577 (1-158)

Qy 32 TCATCAACATCTTCCACCAGTACT 55
|||||
Db 102 SerSerThrSerSerThrSerThr 109

RESULT 13

Q94597

ID Q94597 PRELIMINARY; PRT; 225 AA.

AC Q94597;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE MK35 lipoprotein precursor.

OS Mycobacterium kansasii.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1768;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bostrom;

RX MEDLINE=96036229; PubMed=7582031;

RA Armoa G.R., Rouse D.A., Nair J., Mackall J.C., Morris S.L.;

RT "A highly immunogenic putative Mycobacterium kansasii lipoprotein.";

RL Microbiology 141:2705-2712(1995).

DR EMBL; U20446; AAA90989.1; -.

KW Lipoprotein; Signal.

FT SIGNAL 6 13 Potential.

FT CHAIN 14 225 MK35 lipoprotein.

SQ SEQUENCE 225 AA; 23083 MW; F5E90E23CCCAAB4D CRC64;

Alignment Scores:

Pred. No.: 55.4 Length: 225

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 8.70% Indels: 0

DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q49597 (1-225)

Qy 32 TCATCAACATCTTCCACCAGTACT 55
|||||
Db 34 SerSerThrSerSerThrSerThr 41

RESULT 14

Q20587

ID Q20587 PRELIMINARY; PRT; 275 AA.

AC Q20587;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein F49C12.10.

GN ORFNames=F49C12.10;

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for investigating biology.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Gardner A.E.;

RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z68227; CAA92513.1; -.

DR PIR; T22414; T22414.

DR WormBase; WBGene00009879; F49C12.10.

DR WormPep; F49C12.10; CE03370.

KW Hypothetical protein.

SQ SEQUENCE 275 AA; 32355 MW; 5CDD0DECE7381F9E CRC64;

Alignment Scores:

Pred. No.: 54.2 Length: 275

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 8.70% Indels: 0

DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q20587 (1-275)

Qy 51 GTACTCCGTTCCGGTGGGCATTT 74

Db 174 ValLeuArgSerGlyGlyAlaPhe 181
|||||
RESULT 15
Q7MSF1 PRELIMINARY; PRT; 319 AA.
AC Q7MSF1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=WS0523;
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSMZ 1740;
RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
DR EMBL; BX571658; CAE09660.1; -.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR PROSITE; PS0293; TPR_REGION; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 319 AA; 35080 MW; 6BDBF2D78D87DEB4 CRC64;

Alignment Scores:
Pred. No.: 53.2 Length: 319
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q7MSF1 (1-319)

Qy 74 TCGACACCCCTCAACAAGCGTGAGC 97
|||||
Db 15 SerThrProSerThrSerValSer 22

Search completed: February 23, 2005, 11:49:08
Job time : 134 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:23:55 ; Search time 113.5 Seconds
(without alignments)
1880.984 Million cell updates/sec

Title: US-09-910-208B-1
Perfect score: 92
Sequence: 1 atgactaagctggaagatca.....acatagatatccacaaagag 276

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Word size: 1
Total number of hits satisfying chosen parameters: 3967864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/HADDAD-09-910208/runat_23022005_101828_14945/app_query.fasta_1.
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=oligo.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208 @CGN 1 1 224 @runat_23022005_101828_14945 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	92	2	AAW03563 Calcium b
2	90	97.8	90	3	AAY90765 Bovine CA
3	90	97.8	90	3	AAY90764 Bovine co
4	20	21.7	91	2	AAW01826 Component
5	20	21.7	91	2	AAW93819 Angiotrop
6	18	19.6	18	3	AAY90766 Endo Lys
7	15	16.3	30	2	AAR85169 Bovine se
8	15	16.3	50	3	AAY90763 Human EN-
9	9	9.8	46	4	ABB43183 Peptide #
10	9	9.8	46	4	AAM37021 Peptide #

C 84	7	7.6	103	5	ABP69193	Abp69193 Human pol	C 157	7	7.6	309	4	AAU24751	Aau24751 Human olf
C 85	7	7.6	104	6	ADA57076	Ada57076 Human sec	C 158	7	7.6	309	5	ABG76845	Abg76845 Human G-p
C 86	7	7.6	104	6	ADA40928	Ada40928 Human sec	C 159	7	7.6	309	5	ABB54573	Abb54573 Lactococc
C 87	7	7.6	104	7	ADD37928	Add37928 Human sec	C 160	7	7.6	309	5	AAU85371	Aau85371 G-coupled
C 88	7	7.6	105	2	AAW88615	Aaw88615 Secreted	C 161	7	7.6	310	3	AAG23168	Aag23168 Arabidops
C 89	7	7.6	105	4	ABB50382	Abb50382 Human sec	C 162	7	7.6	310	3	AAG45838	Aag45838 Arabidops
C 90	7	7.6	105	6	ABO44639	AbO44639 Novel hum	C 163	7	7.6	310	6	ABP97070	Abp97070 Human G p
C 91	7	7.6	105	7	ABO26119	AbO26119 Human pro	C 164	7	7.6	310	7	ADC85653	Adc85653 Human GPC
C 92	7	7.6	109	8	ADQ65397	Adq65397 Novel hum	C 165	7	7.6	310	7	ADG84279	Adg84279 Human TMD
C 93	7	7.6	117	7	ADF59399	Adf59399 Human pol	C 166	7	7.6	312	5	ABP40738	Abp40738 Staphyloc
C 94	7	7.6	123	5	ADK35204	Adk35204 Novel hum	C 167	7	7.6	312	8	ADS08044	Ads08044 Staphyloc
C 95	7	7.6	135	4	ABB71040	Abb71040 Drosophil	C 168	7	7.6	315	5	ABG77246	Abg77246 Selected
C 96	7	7.6	137	4	AAO06256	Aao06256 Human pol	C 169	7	7.6	318	6	ABU49698	Abu49698 Protein e
C 97	7	7.6	138	4	AAU31239	Aau31239 Novel hum	C 170	7	7.6	320	4	AAU67615	Aau67615 Propionib
C 98	7	7.6	164	5	AAE20651	Aae20651 Human gen	C 171	7	7.6	320	6	ABM64976	Abm64976 Propionib
C 99	7	7.6	170	4	AAG71888	Aag71888 Human olf	C 172	7	7.6	320	6	ABM64134	Abm64134 Propionib
C 100	7	7.6	176	8	ABO58920	AbO58920 Human gen	C 173	7	7.6	320	8	ADR68708	Adr68708 Penicilli
C 101	7	7.6	179	2	AAW80659	Aaw80659 S. pneumo	C 174	7	7.6	325	3	AAG45837	Aag45837 Arabidops
C 102	7	7.6	183	7	ADC95884	Adc95884 E. faeciu	C 175	7	7.6	325	3	AAG23167	Aag23167 Arabidops
C 103	7	7.6	186	4	ABB69467	Abb69467 Drosophil	C 176	7	7.6	327	5	ADI16806	Adi16806 Human NOV
C 104	7	7.6	194	4	AAU19319	Aau19319 Human G p	C 177	7	7.6	327	5	ADI16498	Adi16498 Human NOV
C 105	7	7.6	200	7	ABO78511	AbO78511 Pseudomon	C 178	7	7.6	327	6	ABM82856	Abm82856 NIT relat
C 106	7	7.6	204	4	ABU52951	Abu52951 Human tra	C 179	7	7.6	327	6	ABM65919	Abm65919 Propionib
C 107	7	7.6	204	7	ADH85669	Adh85669 Enterococ	C 180	7	7.6	331	4	AAU51834	Aau51834 Propionib
C 108	7	7.6	210	3	AAB44543	Aab44543 Virulence	C 181	7	7.6	331	6	ABM48353	Abm48353 Propionib
C 109	7	7.6	210	5	ABP54495	Abp54495 Pasteurel	C 182	7	7.6	334	8	ADS27736	Ads27736 Bacterial
C 110	7	7.6	212	6	AAU37626	Aau37626 Streptoco	C 183	7	7.6	338	4	ABG01710	Abg01710 Novel hum
C 111	7	7.6	212	6	ABU45820	Abu45820 Protein e	C 184	7	7.6	340	5	ABP58974	Abp58974 Human i k
C 112	7	7.6	224	3	AAB57054	Aab57054 Human pro	C 185	7	7.6	347	4	ABB50177	Abb50177 Human tra
C 113	7	7.6	226	6	ABU69133	Abu69133 Human NOV	C 186	7	7.6	347	7	ADB64690	Adb64690 Human pro
C 114	7	7.6	226	8	ADO08269	Ado08269 Human NOV	C 187	7	7.6	347	7	ADC31185	Adc31185 Human nov
C 115	7	7.6	227	7	ABO81633	AbO81633 Pseudomon	C 188	7	7.6	347	8	ADR08626	Adr08626 Human pro
C 116	7	7.6	231	7	ABO68943	AbO68943 Pseudomon	C 189	7	7.6	349	8	ADJ49117	Adj49117 Oil-assoc
C 117	7	7.6	236	7	ABO80020	AbO80020 Pseudomon	C 190	7	7.6	349	8	ADJ50144	Adj50144 Oil-assoc
C 118	7	7.6	243	7	ADD11648	Add11648 Arabidops	C 191	7	7.6	350	7	ADM03905	Adm03905 Human pro
C 119	7	7.6	243	7	ADD30318	Add30318 Plant yie	C 192	7	7.6	351	8	ADH58986	Adh58986 Mouse GPC
C 120	7	7.6	243	8	ADI44237	Adi44237 Plant tra	C 193	7	7.6	351	8	ADI53333	Adi53333 Mouse FPR
C 121	7	7.6	245	8	ADR16225	Adr16225 Streptoco	C 194	7	7.6	351	8	ADO29714	Ado29714 Mouse GPC
C 122	7	7.6	245	8	ADS30320	Ads30320 Bacterial	C 195	7	7.6	351	8	ADO57850	Ado57850 Mouse for
C 123	7	7.6	249	6	ABU28502	Abu28502 Protein e	C 196	7	7.6	399	7	ABO77270	AbO77270 Pseudomon
C 124	7	7.6	250	4	ABG12917	Abg12917 Novel hum	C 197	7	7.6	402	7	ABO78963	AbO78963 Pseudomon
C 125	7	7.6	254	6	ABU06072	Abu06072 N. mening	C 198	7	7.6	407	5	ABB09999	Abb09999 Human pro
C 126	7	7.6	255	4	ABB69299	Abb69299 Drosophil	C 199	7	7.6	407	5	ABG64626	Abg64626 Human alb
C 127	7	7.6	255	6	AAE37037	Aae37037 Human nuc	C 200	7	7.6	407	8	ADL77893	Adl77893 Albumin f
C 128	7	7.6	257	6	ABP78820	Abp78820 N. gonorr	C 201	7	7.6	418	7	ABO83887	AbO83887 Pseudomon
C 129	7	7.6	263	4	AAU62592	Aau62592 Propionib	C 202	7	7.6	424	4	ABB64620	Abb64620 Drosophil
C 130	7	7.6	263	6	ABM59111	Abm59111 Propionib	C 203	7	7.6	426	4	ABB65845	Abb65845 Drosophil
C 131	7	7.6	264	3	AAG40069	Aag40069 Arabidops	C 204	7	7.6	434	6	ADA57216	Ada57216 Human sec
C 132	7	7.6	264	3	AAG04977	Aag04977 Arabidops	C 205	7	7.6	434	6	ADA41095	Ada41095 Human sec
C 133	7	7.6	264	5	ABG32883	Abg32883 Human zlm	C 206	7	7.6	434	7	ADB91664	Adb91664 Human sec
C 134	7	7.6	270	6	ABU17017	Abu17017 Protein e	C 207	7	7.6	438	4	AAU33707	Aau33707 Pseudomon
C 135	7	7.6	270	6	ADB07000	Adb07000 Alloiococ	C 208	7	7.6	438	6	ABU15597	Abu15597 Protein e
C 136	7	7.6	270	7	ADH85668	Adh85668 Enterococ	C 209	7	7.6	441	4	AAG91857	Aag91857 C glutami
C 137	7	7.6	271	4	AAG90190	Aag90190 C glutami	C 210	7	7.6	442	4	AAG65742	Aag65742 Flea epox
C 138	7	7.6	271	6	ABR43441	AbR43441 Human mal	C 211	7	7.6	442	4	AAB51012	Aab51012 Flea epox
C 139	7	7.6	271	7	ADI21201	Adi21201 Novel hum	C 212	7	7.6	446	5	ABJ11117	Abj11117 Yeast sel
C 140	7	7.6	272	3	AAG29929	Aag29929 Arabidops	C 213	7	7.6	456	5	ABB91513	Abb91513 Herbicida
C 141	7	7.6	282	3	AAG04976	Aag04976 Arabidops	C 214	7	7.6	456	8	ADR16242	Adr16242 Streptoco
C 142	7	7.6	282	3	AAG40068	Aag40068 Arabidops	C 215	7	7.6	460	1	AAP81061	Aap81061 Sequence
C 143	7	7.6	289	5	ABG76864	Abg76864 Human G-p	C 216	7	7.6	464	2	AAY24003	Aay24003 A flea ep
C 144	7	7.6	292	6	ADA34549	Ada34549 Acinetoba	C 217	7	7.6	464	2	AAY24004	Aay24004 A flea ep
C 145	7	7.6	296	6	ABU65257	Abu65257 Novel hum	C 218	7	7.6	464	3	AAY68739	Aay68739 Amino aci
C 146	7	7.6	301	4	ABB59924	Abb59924 Drosophil	C 219	7	7.6	464	4	AAB36983	Aab36983 Protein s
C 147	7	7.6	302	4	ABG10947	Abg10947 Novel hum	C 220	7	7.6	464	4	AAB36982	Aab36982 Flea epox
C 148	7	7.6	303	4	AAU33897	Aau33897 Staphyloc	C 221	7	7.6	464	4	AAG65736	Aag65736 Flea epox
C 149	7	7.6	306	4	AAU36707	Aau36707 Staphyloc	C 222	7	7.6	464	4	AAG65735	Aag65735 Flea epox
C 150	7	7.6	306	6	ADA89524	Ada89524 Staphyloc	C 223	7	7.6	464	4	AAB51005	Aab51005 Flea epox
C 151	7	7.6	306	6	ABU16314	Abu16314 Protein e	C 224	7	7.6	464	4	AAB51006	Aab51006 Flea epox
C 152	7	7.6	306	6	ABU42743	Abu42743 Protein e	C 225	7	7.6	470	6	ABR40853	Abr40853 Catalpa s
C 153	7	7.6	306	6	ABU44001	Abu44001 Protein e	C 226	7	7.6	474	3	AAB34722	Aab34722 Human sec
C 154	7	7.6	306	6	ABM72329	Abm72329 Staphyloc	C 227	7	7.6	475	8	ADS43662	Ads43662 Bacterial
C 155	7	7.6	308	6	ADA83766	Ada83766 Human SLC	C 228	7	7.6	483	7	ABO70478	AbO70478 Pseudomon
C 156	7	7.6	308	8	ADP25135	Adp25135 PRO polyp	C 229	7	7.6	485	5	ABP69693	Abp69693 Human pol

C 230	7	7.6	500	6	AAE30796	Aae30796 Human tra	303	7	7.6	674	8	ADL15347	Adl15347 B thuring
C 231	7	7.6	503	7	ABO83917	Abo83917 Pseudomon	304	7	7.6	675	8	ADL15377	Adl15377 B thuring
232	7	7.6	504	3	AAB44568	Ab44568 Virulence	305	7	7.6	675	8	ADL15351	Adl15351 B thuring
233	7	7.6	504	5	ABP54520	Abp54520 Pasteurel	306	7	7.6	675	8	ADL15349	Adl15349 B thuring
234	7	7.6	504	8	ADS17616	Adsl7616 Amino aci	307	7	7.6	675	8	ADL15345	Adl15345 B thuring
235	7	7.6	505	8	ADG73740	Adg73740 Aspergill	308	7	7.6	675	8	ADL15381	Adl15381 B thuring
236	7	7.6	506	5	ABB91594	Abb91594 Herbicida	309	7	7.6	675	8	ADL15383	Adl15383 B thuring
237	7	7.6	519	4	ABG07249	Abg07249 Novel hum	C 310	7	7.6	675	8	ADN20157	Adn20157 Bacterial
238	7	7.6	529	4	AAB81926	Aab81926 Acremoniu	311	7	7.6	676	8	ADL15343	Adl15343 B thuring
239	7	7.6	533	3	AAY93953	Aay93953 Amino aci	312	7	7.6	676	8	ADL15375	Adl15375 B thuring
240	7	7.6	533	3	AAY93952	Aay93952 Amino aci	313	7	7.6	677	8	ADL15355	Adl15355 B thuring
241	7	7.6	548	8	ADO61981	Ado61981 Transcrip	314	7	7.6	677	8	ADL15387	Adl15387 B thuring
C 242	7	7.6	548	8	ADS23189	Ads23189 Bacterial	315	7	7.6	687	6	ABR53552	AbR53552 Protein s
C 243	7	7.6	556	8	ADN22789	Adn22789 Bacterial	316	7	7.6	687	7	ADK64396	Adk64396 Disease t
C 244	7	7.6	558	7	ABO78932	Abo78932 Pseudomon	317	7	7.6	692	8	ADR68709	Adr68709 Penicilli
C 245	7	7.6	559	8	ADJ67952	Adj67952 G. stearo	C 318	7	7.6	698	8	ADS21451	Ads21451 Bacterial
C 246	7	7.6	559	8	ADJ68164	Adj68164 G. stearo	319	7	7.6	702	4	AAE01160	Aae01160 Drosophil
C 247	7	7.6	559	8	ADK01242	Adk01242 DNA polym	320	7	7.6	702	4	ABB71509	Abb71509 Drosophil
C 248	7	7.6	559	8	ADJ79461	Adj79461 G. stearo	C 321	7	7.6	714	6	AAO31003	Aao31003 Human tra
C 249	7	7.6	559	8	ADJ84901	Adj84901 B. steart	C 322	7	7.6	714	8	ADR09688	Adr09688 Human pro
C 250	7	7.6	559	8	ADM77689	Adm77689 DNA polym	C 323	7	7.6	717	4	ABB60361	Abb60361 Drosophil
C 251	7	7.6	559	8	ADM66356	Adm66356 G. stearo	C 324	7	7.6	730	6	ABU12299	Abu12299 Human aut
C 252	7	7.6	559	8	ADO04409	Ado04409 B. steart	325	7	7.6	786	7	ADE57208	Ade57208 Rat Prote
C 253	7	7.6	559	8	ADP82486	Adp82486 B. stearo	326	7	7.6	786	7	ADE57204	Ade57204 Rat Prote
C 254	7	7.6	563	8	ADR50793	Adr50793 Human c-b	C 327	7	7.6	812	6	ABM68038	Abm68038 Photorhab
C 255	7	7.6	571	4	ABB62038	Abb62038 Drosophil	328	7	7.6	837	4	ABB68265	Abb68265 Drosophil
256	7	7.6	583	4	ABG09959	Abg09959 Novel hum	C 329	7	7.6	848	6	ADA38354	Ada38354 Vibrio ha
257	7	7.6	602	8	ADS43991	Ads43991 Bacterial	330	7	7.6	859	4	ABB71182	Abb71182 Drosophil
C 258	7	7.6	609	7	ADJ70515	Adj70515 Human hea	331	7	7.6	860	8	ADL04498	Adl04498 M. catarr
C 259	7	7.6	613	8	ADJ35082	Adj35082 Xylanase	C 332	7	7.6	861	6	ABU12316	Abu12316 Human PAT
261	7	7.6	635	7	ADE61270	Ade61270 Rat Prote	333	7	7.6	864	2	AAU03636	Aay03636 Hypoxia-r
262	7	7.6	644	2	AAW13821	Aaw13821 Yeast tra	334	7	7.6	864	6	ABU63755	Abu63755 Rat prote
C 263	7	7.6	646	5	AAO20518	Aao20518 Protein o	335	7	7.6	864	7	ADC69799	Adc69799 Rat neuro
C 264	7	7.6	651	6	ABG74687	Abg74687 Human CGD	336	7	7.6	864	7	ABW01151	Abw01151 Hypoxia-r
265	7	7.6	655	4	AAB70771	Aab70771 Murine ne	337	7	7.6	877	6	ABR53890	AbR53890 Protein s
C 266	7	7.6	657	7	ABO79255	Abo79255 Pseudomon	338	7	7.6	877	7	ADK64848	Adk64848 Disease t
267	7	7.6	663	8	ADQ08650	Adq08650 Ciona int	C 339	7	7.6	894	6	ADB12663	Adb12663 Alloiococ
268	7	7.6	667	5	AAU99258	Aau99258 Bacillus	C 340	7	7.6	895	6	ABU12304	Abu12304 Human PAT
269	7	7.6	667	5	AAU99257	Aau99257 Bacillus	C 341	7	7.6	901	6	ADB12661	Adb12661 Alloiococ
270	7	7.6	669	5	AAU99259	Aau99259 Maize Opt	343	7	7.6	922	3	AAB36515	Aab36515 Candida a
271	7	7.6	669	5	AAU99262	Aau99262 Bacillus	344	7	7.6	922	5	ABP73838	Abp73838 Candida a
272	7	7.6	669	8	ADL15309	Adl15309 B thuring	C 345	7	7.6	933	6	ABU12307	Abu12307 Human PAT
273	7	7.6	669	8	ADL15315	Adl15315 B thuring	C 346	7	7.6	938	6	ADB12659	Adb12659 Alloiococ
274	7	7.6	670	5	AAU99273	Aau99273 Bacillus	C 347	7	7.6	949	8	ADM87258	Adm87258 Human pro
275	7	7.6	670	5	AAU99266	Aau99266 Bacillus	C 348	7	7.6	958	3	AAU51120	Aay51120 Human SAR
276	7	7.6	673	5	AAU99265	Aau99265 Bacillus	349	7	7.6	958	8	ADL83102	Adl83102 Human PRO
277	7	7.6	673	5	AAU99271	Aau99271 Bacillus	C 350	7	7.6	965	7	ADC31607	Adc31607 Human nov
278	7	7.6	673	5	AAU99263	Aau99263 Bacillus	351	7	7.6	982	4	ABB59353	Abb59353 Drosophil
279	7	7.6	673	5	AAU99260	Aau99260 Bacillus	C 352	7	7.6	982	4	ABB67401	Abb67401 Drosophil
280	7	7.6	673	8	ADL15325	Adl15325 B thuring	353	7	7.6	993	6	ABU12300	Abu12300 Human PAT
281	7	7.6	673	8	ADL15393	Adl15393 B thuring	354	7	7.6	1013	4	ABB60789	Abb60789 Drosophil
282	7	7.6	673	8	ADL15317	Adl15317 B thuring	C 355	7	7.6	1023	6	ABU48443	Abu48443 Protein e
283	7	7.6	673	8	ADL15365	Adl15365 B thuring	C 356	7	7.6	1024	5	ABB04861	Abb04861 LDL recep
284	7	7.6	673	8	ADL15337	Adl15337 B thuring	C 357	7	7.6	1026	6	ABU12314	Abu12314 Human PAT
285	7	7.6	673	8	ADL15389	Adl15389 B thuring	C 358	7	7.6	1031	4	AAU35339	Aau35339 Enterococ
286	7	7.6	673	8	ADL15311	Adl15311 B thuring	C 359	7	7.6	1044	6	ABU12310	Abu12310 Human PAT
287	7	7.6	673	8	ADL15333	Adl15333 B thuring	360	7	7.6	1061	6	ABU29451	Abu29451 Protein e
288	7	7.6	673	8	ADL15371	Adl15371 B thuring	361	7	7.6	1077	4	ABB58720	Abb58720 Drosophil
289	7	7.6	673	8	ADL15361	Adl15361 B thuring	362	7	7.6	1083	8	ADM87238	Adm87238 Human pro
290	7	7.6	673	8	ADL15369	Adl15369 B thuring	363	7	7.6	1157	2	AAR28900	Aar28900 Toxin 50C
291	7	7.6	673	8	ADL15391	Adl15391 B thuring	364	7	7.6	1157	2	AAR25997	Aar25997 Delta-end
292	7	7.6	673	8	ADL15395	Adl15395 B thuring	365	7	7.6	1157	2	AAR27343	Aar27343 B.thuring
293	7	7.6	673	8	ADL15367	Adl15367 B thuring	366	7	7.6	1157	2	AAR44208	Aar44208 Bacillus
294	7	7.6	673	8	ADL15357	Adl15357 B thuring	367	7	7.6	1157	2	AAW06418	Aaw06418 Antiscara
295	7	7.6	673	8	ADL15373	Adl15373 B thuring	368	7	7.6	1157	8	ADR89430	Adr89430 cry8Aa. 1
296	7	7.6	673	8	ADL15397	Adl15397 B thuring	369	7	7.6	1169	2	AAW06417	Aaw06417 Antiscara
297	7	7.6	673	8	ADL15329	Adl15329 B thuring	370	7	7.6	1193	7	ADJ70742	Adj70742 Human hea
298	7	7.6	673	8	ADL15359	Adl15359 B thuring	371	7	7.6	1206	5	AAU99255	Aau99255 Bacillus
299	7	7.6	673	8	ADL15363	Adl15363 B thuring	372	7	7.6	1206	8	ADL15305	Adl15305 B thuring
300	7	7.6	674	8	ADL15385	Adl15385 B thuring	373	7	7.6	1210	5	AAU99256	Aau99256 Bacillus
301	7	7.6	674	8	ADL15379	Adl15379 B thuring	374	7	7.6	1210	8	ADL15307	Adl15307 B thuring
302	7	7.6	674	8	ADL15353	Adl15353 B thuring	375	7	7.6	1222	8	ADR39771	Adr39771 Human kin

376	7	7.6	1248	2	AAW19783	Aaw19783 Human mul
377	7	7.6	1384	8	ADN61482	Adn61482 Human KPP
378	7	7.6	1392	8	ADJ96675	Adj96675 Human pro
379	7	7.6	1468	4	ABB65329	Abb65329 Drosophil
380	7	7.6	1551	4	ABB64459	Abb64459 Drosophil
381	7	7.6	1603	5	ABB81171	Abb81171 Human put
382	7	7.6	1603	8	ADJ57844	Adj57844 MRB prote
383	7	7.6	1655	4	ABG17466	Abg17466 Novel hum
384	7	7.6	1726	2	AAW19784	Aaw19784 Human mul
385	7	7.6	1726	7	ADB79869	Adb79869 Rat putat
386	7	7.6	1759	5	ABP69142	Abp69142 Human pol
387	7	7.6	1784	8	ADR86368	Adr86368 Aspergill
388	7	7.6	2000	7	ADK62360	Adk62360 Disease t
389	7	7.6	2015	4	ABB65890	Abb65890 Drosophil
390	7	7.6	2164	1	AAP81045	Aap81045 Sequence
391	7	7.6	2164	1	AAP80131	Aap80131 Peptides
392	7	7.6	2182	2	AAW22476	Aaw22476 Plasmodiu
393	7	7.6	2182	3	AAW77906	Aay77906 Plasmodiu
394	7	7.6	2285	2	AAW98149	Aaw98149 Bacillus
395	7	7.6	2870	3	AAy95559	Aay95559 Caenorhab
396	7	7.6	2870	8	ADN07634	Adn07634 Caenorhab
397	7	7.6	3178	3	AAy95556	Aay95556 Caenorhab
398	7	7.6	3178	8	ADN07623	Adn07623 Caenorhab
399	7	7.6	4315	5	ABP43908	Abp43908 MUC5B par
400	7	7.6	4773	7	ADJ95094	Adj95094 Novel NOV
401	7	7.6	5703	8	ADL23265	Adl23265 Human MUC
402	6	6.5	8	4	AAB48902	Aab48902 TGAT SECI
403	6	6.5	8	7	ADB61382	Adb61382 Rheumatoi
404	6	6.5	9	4	AAU24260	Aau24260 Human MHC
405	6	6.5	9	4	AAU24062	Aau24062 Human MHC
406	6	6.5	9	4	AAU24037	Aau24037 Human MHC
407	6	6.5	9	4	AAU23943	Aau23943 Human MHC
408	6	6.5	9	4	AAU24352	Aau24352 Human MHC
409	6	6.5	9	5	ABP47393	Abp47393 N. mening
410	6	6.5	9	5	ABP47397	Abp47397 N. mening
411	6	6.5	9	5	ABP47417	Abp47417 N. mening
412	6	6.5	9	5	ABP47376	Abp47376 N. mening
413	6	6.5	9	5	ABP47513	Abp47513 N. mening
414	6	6.5	9	5	ABP47402	Abp47402 N. mening
415	6	6.5	9	8	ADN64071	Adn64071 HLA bindi
416	6	6.5	10	2	AAW25923	Aaw25923 Beta-2-mi
417	6	6.5	10	2	AAW25908	Aaw25908 Beta-2-mi
418	6	6.5	10	4	AAU24411	Aau24411 Human MHC
419	6	6.5	10	4	AAU24111	Aau24111 Human MHC
420	6	6.5	10	4	AAU24287	Aau24287 Human MHC
421	6	6.5	10	4	AAU24081	Aau24081 Human MHC
422	6	6.5	10	4	AAU24307	Aau24307 Human MHC
423	6	6.5	10	4	AAU24414	Aau24414 Human MHC
424	6	6.5	10	4	AAU23974	Aau23974 Human MHC
425	6	6.5	10	6	ABP76422	Abp76422 Peptidomi
426	6	6.5	10	6	ADA09381	Ada09381 Haemophil
427	6	6.5	10	7	ADF29001	Adf29001 beta-cate
428	6	6.5	10	8	ADN64064	Adn64064 HLA bindi
429	6	6.5	10	8	ADN64063	Adn64063 HLA bindi
430	6	6.5	10	8	ADR46798	Adr46798 H. influe
431	6	6.5	11	2	AAR55647	Aar55647 GGF segme
432	6	6.5	11	2	AAR55772	Aar55772 GGF segme
433	6	6.5	11	2	AAR55813	Aar55813 GGF segme
434	6	6.5	11	2	AAR46907	Aar46907 GGF segme
435	6	6.5	11	2	AAR67235	Aar67235 Bovine gl
436	6	6.5	11	2	AAR96067	Aar96067 Glial gro
437	6	6.5	11	2	AAW09353	Aaw09353 Human gli
438	6	6.5	11	2	AAy26567	Aay26567 Bovine an
439	6	6.5	11	5	ABP47653	Abp47653 N. mening
440	6	6.5	11	6	ABP70595	Abp70595 Human pap
441	6	6.5	11	6	ABP98787	Abp98787 Peptide #
442	6	6.5	12	8	ADJ82927	Adj82927 Mycobacte
443	6	6.5	13	2	AAR14753	Aar14753 Seroreact
444	6	6.5	13	5	ADG67435	Adg67435 Mouse ant
445	6	6.5	13	5	ADG67509	Adg67509 Humanised
446	6	6.5	13	5	ADG67434	Adg67434 Mouse ant
447	6	6.5	13	5	ADG67508	Adg67508 Humanised
448	6	6.5	14	3	AAB24011	Aab24011 Partial p

449	6	6.5	14	3	ADC16845	Adc16845 Human sin
450	6	6.5	14	7	ADO70233	Ado70233 Human GPA
451	6	6.5	15	2	AAW47391	Aaw47391 Spruce bu
C 452	6	6.5	15	2	AAy33077	Aay33077 Carbohydr
C 453	6	6.5	15	2	AAy01479	Aay01479 N-termina
C 454	6	6.5	15	2	AAy14549	Aay14549 Rat LSR-g
455	6	6.5	15	3	AAy49463	Aay49463 Spruce bu
456	6	6.5	15	5	AAO15974	Aao15974 Human mac
457	6	6.5	15	5	ABB80709	Abb80709 Thermal h
C 458	6	6.5	15	6	ABU87162	Abu87162 Carbohydr
459	6	6.5	15	7	ADF09362	Adf09362 Human cal
460	6	6.5	15	8	ADN65117	Adn65117 HLA bindi
461	6	6.5	15	8	ADR19434	Adr19434 TRPI deri
462	6	6.5	16	2	AAR52159	Aar52159 Mouse lig
463	6	6.5	17	2	AAR51112	Aar51112 N-termina
C 464	6	6.5	17	7	ADD36497	Add36497 NRIF3 C-t
465	6	6.5	20	2	AAR04992	Aar04992 Papilloma
C 466	6	6.5	20	2	AAW76825	Aaw76825 Xenopus s
C 467	6	6.5	20	2	AAW76824	Aaw76824 Human CTN
C 468	6	6.5	20	4	AAy72830	Aay72830 Human bet
C 469	6	6.5	20	4	AAy72828	Aay72828 Human bet
C 470	6	6.5	20	4	AAy72826	Aay72826 Xenopus b
C 471	6	6.5	20	4	AAy72785	Aay72785 Human bet
472	6	6.5	20	5	AAO18146	Aao18146 HPV type
473	6	6.5	20	5	AAO18147	Aao18147 HPV type
474	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
475	6	6.5	20	5	ABP47326	Abp47326 HPV18 E7
476	6	6.5	23	2	AAy36599	Aay36599 Fragment
C 477	6	6.5	23	3	AAy69801	Aay69801 HIV-1 gp4
C 478	6	6.5	23	4	AAB98277	Aab98277 Anti-A33
C 479	6	6.5	23	4	AAB98276	Aab98276 Anti-A33
C 480	6	6.5	23	4	AAB97656	Aab97656 A33 antiig
C 481	6	6.5	23	4	AAB97657	Aab97657 A33 antiig
482	6	6.5	23	6	ADA11769	Ada11769 Human nov
C 483	6	6.5	23	8	ADO10370	Ado10370 HIV1 glyc
C 484	6	6.5	25	8	ADR13994	Adr13994 NGR ligan
485	6	6.5	26	2	AAR52371	Aar52371 Mouse hea
486	6	6.5	26	2	AAR52372	Aar52372 Mouse hea
C 487	6	6.5	27	2	AAR28114	Aar28114 Ionophore
C 488	6	6.5	27	2	AAR27927	Aar27927 Amphiphil
C 489	6	6.5	27	2	AAW66478	Aaw66478 Amphiphil
C 490	6	6.5	28	3	AAy88746	Aay88746 Core poly
C 491	6	6.5	28	4	AAAB77101	Aab77101 Core poly
C 492	6	6.5	28	4	ABB00105	Abb00105 Viral DPl
C 493	6	6.5	28	4	ABB01570	Abb01570 Viral cor
C 494	6	6.5	28	4	AAU12654	Aau12654 DPl78-lik
C 495	6	6.5	28	5	ADE01590	Ade01590 Hybrid po
496	6	6.5	29	2	AAR68587	Aar68587 Human pro
497	6	6.5	29	2	AAR68587	Aar68587 Human pro
498	6	6.5	30	2	AAR15585	Aar15585 Immunopep
C 499	6	6.5	30	5	AAE23961	Aae23961 Beta-cate
C 500	6	6.5	30	7	ADG63050	Adg63050 Human atr

ALIGNMENTS

RESULT 1

AAW03563

ID AAW03563 standard; protein; 92 AA.

XX

AC AAW03563;

XX 01-MAY-1997 (first entry)

XX

DE Calcium binding protein CAAAF1.

XX

KW Calcium binding protein; bovine; amniotic fluid; s100 protein family;
KW intracellular signal transduction; squamous epithelial cell; neutrophil;
KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW squamous cell carcinoma; skin; oesophagus; CAAAF1; lung; blood disease.

OS Bos taurus.

XX

PN	EP731166-A2;	PI	Hitomi J, Yamaguchi K, Yamamura T, Kimura T;
XX		PI	
PD	11-SEP-1996;	XX	WPI; 1996-403989/41.
XX		DR	N-PSDB; AAT39345.
PF	04-DEC-1995;	XX	
XX	95EP-00119045.	PT	New human of bovine calcium binding protein and related nucleic acid - is
PR	06-MAR-1995;	PT	a marker for inflammation, neoplasia, skin and blood diseases.
PR	95JP-00045564.	XX	
XX	95JP-00070468.	PS	Claim 1; Page 21; 36pp; English.
PA	(TOFU) TONEN CORP.	CC	This sequence represents the CAAF1 calcium-binding protein isolated from
PA	(HITO/) HITOMI J.	CC	bovine amniotic fluid. CAAF1 belongs to the S100 protein family, which
XX		CC	includes calyculin, MRP8, and MRP14. Intracellular calcium ion
XX		CC	concentration is one of the key factors for intracellular signal
XX		CC	transduction. The calcium signals are transduced by various calcium-
XX		CC	binding proteins, such as the protein encoded by this sequence. CAAF1 is
XX		CC	normally expressed in squamous epithelial cells, neutrophils and
XX		CC	macrophages, but atypical epithelial cells are negative for CAAF1 and
XX		CC	overexpression is observed in several types of cancer cells and
XX		CC	neutrophils/macrophages infiltrating cancerous lesions. Detection of
XX		CC	CAAF1 (using antibodies in usual immunoassays) can be used to diagnose
XX		CC	(or monitor) inflammation, neoplasia (particularly squamous cell
XX		CC	carcinoma of the skin, oesophagus, lung and cervix), and skin and blood
XX		XX	diseases
SQ	Sequence 92 AA;		
Alignment Scores:			
Pred. No.:	1.23e-83	Length:	92
Score:	92.00	Matches:	92
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0
US-09-910-208B-1 (1-276) x AAW03563 (1-92)			
QY	1 ATGACTAAGCTGGAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTACTCCGTT	60	
Db	1 MetThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerVal	20	
QY	61 CGGGTGGGGCATTTTCGACACCCCTCAACAAGCGTGAAGCAGCTGATCACAAGGAA	120	
Db	21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGlu	40	
QY	121 CTTCCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTTCCAAGAC	180	
Db	41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp	60	
QY	181 CTGGATCCGATAAAGCGGAGCCGTCAGCTTTGAGGAATTCGTAGCTGTTCCAGG	240	
Db	61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg	80	
QY	241 GTGCTGAAACAGCCCATAGATATCCACAAGAG	276	
Db	81 ValLeuLysThrAlaHisIleAspIleHisLysGlu	92	
RESULT 2			
AAY90765			
ID	AAY90765 standard; protein; 90 AA.		
XX			
AC	AAY90765;	OS	Bos taurus.
XX		XX	
DT	18-AUG-2000 (first entry)	PN	WO200020621-A1.
XX		XX	
DE	Bovine CAAF1 acid sequence SEQ ID NO:4.	PD	13-APR-2000.
XX		XX	
KW	Bovine; EN-RAGE; extracellular novel RAGE binding protein; receptor for advanced glycation endproduct; inflammation; inhibition; antiinflammatory; immunoglobulin; cell surface molecule; septic shock; systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia; autoimmune disorder; inflammatory disorder.	PF	06-OCT-1999; 99WO-US023303.
XX		XX	
OS		PR	06-OCT-1998; 98US-00167705.
XX		PR	05-MAR-1999; 99US-00263312.
PN	WO200020621-A1.	XX	(UYCO) UNIV COLUMBIA NEW YORK.
XX		PA	Schmidt AM, Stern D;
PD	13-APR-2000.	XX	WPI; 2000-303794/26.
XX		XX	New human EN-RAGE (extracellular novel receptor for advanced glycation
XX		XX	end products) peptide, useful for identifying anti-inflammatory compounds
XX		XX	that inhibit its interaction with RAGE.
XX		XX	Claim 2; Page 41; 132pp; English.
XX		XX	The present invention describes an isolated human EN-RAGE (extracellular
XX		XX	novel receptor for advanced glycation end products) peptide (P1). The EN-
XX		XX	RAGE peptide binds to RAGE which is a member of the immunoglobulin
XX		XX	superfamily of cell-surface molecules. A compound capable of inhibiting
XX		XX	the interaction of EN-RAGE with RAGE is useful for the suppression of
XX		XX	inflammation resulting from systemic lupus erythematosus, inflammatory
XX		XX	lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
XX		XX	inflammatory disorder in which the recruitment of EN-RAGE containing
XX		XX	inflammatory cells occurs. The compound is also useful for the treatment
XX		XX	of systemic lupus erythematosus, inflammatory lupus nephritis in a
XX		XX	subject. The human EN-RAGE peptide is useful for identifying compounds
XX		XX	that inhibit its interaction with RAGE. The present sequence represents
XX		XX	the bovine CAAF1 which shows homology to the human EN-RAGE N-terminal
XX		XX	amino acid sequence
SQ	Sequence 90 AA;		
Alignment Scores:			
Pred. No.:	1.28e-81	Length:	90
Score:	90.00	Matches:	90
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	97.83%	Indels:	0
DB:	3	Gaps:	0
US-09-910-208B-1 (1-276) x AAY90765 (1-90)			
QY	4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTACTCCGTTCCG	63	
Db	1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg	20	
QY	64 GTGGGCGATTTTCGACACCCCTCAACAAGCGTGAAGCAGCTGATCACAAGGAACCTT	123	
Db	21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu	40	
QY	124 CCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTTCCAAGACCTG	183	
Db	41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu	60	

SQ Sequence 91'AA;
Alignment Scores:
Pred. NO.: 4.44e-11 Length: 91
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAW01826 (1-91)

QY 4 ACTAAGCTGGAATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
|||||
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

RESULT 5
AAW93819
ID AAW93819 standard; peptide; 91 AA.
XX
AC AAW93819;
DT 21-JUN-1999 (first entry)
XX
DE Angiotropin related protein derived peptide.
XX
KW Angiotropin related protein; ARP; ternary complex; S100 protein;
KW copper-containing ribonucleoprotein; copper; cell selective;
KW morphogenic action; blood capillary endothelial cell; confluent;
KW non-mitogenic induction; cell phenotype; three-dimensional organoid;
KW spatiotemporal supracellular organisation; chemotropic; blood vessel;
KW tissue neovascularisation; angiogenesis modulation.

OS Synthetic.
XX
PN DE19811047-C1.
XX
PD 15-APR-1999.
XX
PF 13-MAR-1998; 98DE-01011047.
XX
PR 13-MAR-1998; 98DE-01011047.
XX
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI Kieseewetter S, Kuhn E, Koch-Pelster B, Brunner H;
XX WPI; 1999-216114/19.

XX Copper-containing ribonucleoproteins - useful for modulating
PT angiogenesis.
PT
XX

PS Disclosure; Page 2; 16pp; German.

XX This invention describes novel copper-containing ribonucleoproteins which
CC are ternary complexes of an S100 protein, copper ions, and RNA comprising
CC the following consensus sequence or its complement GGAAAUNNNNNUNAUAGN1-
CC 6CUNNUUNNNNNAAN0-1UANAAACAUN0-SCUUNAGN0- 13AGAA-AUN0-16UUAGCAG where
CC N = G, A, U or C. The ribonucleoproteins are stated to have the following
CC properties (1) cell-selective morphogenic action in vitro on isolated
CC primary and/or cloned blood capillary endothelial cells in culture for
CC the non-mitogenic induction of the change in cell phenotype from the
CC confluent state, for non-mitogenic alteration of the spatiotemporal
CC supracellular organisation of cells into three-dimensional organoid,
CC capillary-like structures in culture, (2) a specific chemotropic action
CC on blood vessels in vivo, (3) induction of directional growth of blood
CC vessels in vivo and (4) induction of neovascularisation of tissues
CC through directed ingrowth of blood vessels. Their use for modulating
CC angiogenesis is claimed

XX Sequence 91 AA;

SQ Alignment Scores:

Alignment Scores:
Pred. No.: 5.06e-09 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0

Pred. No.: 4.44e-11 Length: 91
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAW93819 (1-91)

QY 4 ACTAAGCTGGAATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
|||||
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

RESULT 6
AAW90766
ID AAY90766 standard; protein; 18 AA.
XX

AC AAY90766;
XX
DT 18-AUG-2000 (first entry)
XX
DE Endo Lys C amino acid sequence SEQ ID NO:5.

XX Bovine; EN-RAGE; extracellular novel RAGE binding protein;
KW receptor for advanced glycation endproduct; inflammation; inhibition;
KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;
KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;
KW autoimmune disorder; inflammatory disorder.

XX Unidentified.

OS WO200020621-A1.

XX 13-APR-2000.

XX 06-OCT-1999; 99WO-US023303.

PR 06-OCT-1998; 98US-00167705.

PR 05-MAR-1999; 99US-00263312.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Schmidt AM, Stern D;

XX WPI; 2000-303794/26.

PT New human EN-RAGE (extracellular novel receptor for advanced glycation
PT end products) peptide, useful for identifying anti-inflammatory compounds
PT that inhibit its interaction with RAGE.

XX Claim 2; Page 41; 132pp; English.

PS The present invention describes an isolated human EN-RAGE (extracellular
XX novel receptor for advanced glycation end products) peptide (P1). The EN-
CC RAGE peptide binds to RAGE which is a member of the immunoglobulin
CC superfamily of cell-surface molecules. A compound capable of inhibiting
CC the interaction of EN-RAGE with RAGE is useful for the suppression of
CC inflammation resulting from systemic lupus erythematosus, inflammatory
CC lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
CC inflammatory disorder in which the recruitment of EN-RAGE containing
CC inflammatory cells occurs. The compound is also useful for the treatment
CC of systemic lupus erythematosus, inflammatory lupus nephritis in a
CC subject. The human EN-RAGE peptide is useful for identifying compounds
CC that inhibit its interaction with RAGE. The present sequence represents
CC Endo Lys C which shows homology to the human EN-RAGE N-terminal amino
CC acid sequence

SQ Sequence 18 AA;

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.57% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x AAY90766 (1-18)

QY 196 GACGGAGCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCACGGTGCTGAAA 249
AAR85169
ID AAR85169 standard; peptide; 30 AA.
XX
AC AAR85169;
XX
DT 06-JUN-1996 (first entry)
XX
DE Bovine serum heparin binding protein (SHBP)-10 N-terminal peptide.
XX
KW N-terminal peptide; bovine; serum heparin binding protein; SHBP-10;
KW fibroblast growth promoter; wound treating agent.
XX
OS Bos taurus.
XX
PN JP07267993-A.
XX
PD 17-OCT-1995.
XX
PF 31-MAR-1994; 94JP-00061904.
XX
PR 31-MAR-1994; 94JP-00061904.
XX
PA (FARH) HOECHST JAPAN KK.
XX
DR WPI; 1995-390281/50.
XX
PT Serum heparin binding protein (SHBP)-10 - is a fibroblast growth
PT promoting protein, useful as a wound-treating agent.
XX
PS Claim 1; Page 4; 4pp; Japanese.
XX
CC The present N-terminal peptide is from the bovine serum heparin binding
CC protein (SHBP)-10. SHBP-10 has a mol. wt. of about 8-12 kDa by SDS-PAGE
CC under reducing conditions, fibroblast growth promoting activity, and is
CC useful as a wound treating agent
XX
SQ Sequence 30 AA;

Alignment Scores:
Pred. No.: 5.18e-06 Length: 30
Score: 15.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.30% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAR85169 (1-30)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCAC 48
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHis 15

RESULT 8
AAY90763
ID AAY90763 standard; protein; 50 AA.
XX
AC AAY90763;
XX
DT 18-AUG-2000 (first entry)
XX
DE Human EN-RAGE N-terminal amino acid sequence SEQ ID NO:2.
XX

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.57% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x AAY90766 (1-18)

QY 196 GACGGAGCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCACGGTGCTGAAA 249
AAR85169
ID AAR85169 standard; peptide; 30 AA.
XX
AC AAR85169;
XX
DT 06-JUN-1996 (first entry)
XX
DE Bovine serum heparin binding protein (SHBP)-10 N-terminal peptide.
XX
KW N-terminal peptide; bovine; serum heparin binding protein; SHBP-10;
KW fibroblast growth promoter; wound treating agent.
XX
OS Bos taurus.
XX
PN JP07267993-A.
XX
PD 17-OCT-1995.
XX
PF 31-MAR-1994; 94JP-00061904.
XX
PR 31-MAR-1994; 94JP-00061904.
XX
PA (FARH) HOECHST JAPAN KK.
XX
DR WPI; 1995-390281/50.
XX
PT Serum heparin binding protein (SHBP)-10 - is a fibroblast growth
PT promoting protein, useful as a wound-treating agent.
XX
PS Claim 1; Page 4; 4pp; Japanese.
XX
CC The present N-terminal peptide is from the bovine serum heparin binding
CC protein (SHBP)-10. SHBP-10 has a mol. wt. of about 8-12 kDa by SDS-PAGE
CC under reducing conditions, fibroblast growth promoting activity, and is
CC useful as a wound treating agent
XX
SQ Sequence 30 AA;

Alignment Scores:
Pred. No.: 5.18e-06 Length: 30
Score: 15.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.30% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAR85169 (1-30)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCAC 48
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHis 15

RESULT 8
AAY90763
ID AAY90763 standard; protein; 50 AA.
XX
AC AAY90763;
XX
DT 18-AUG-2000 (first entry)
XX
DE Human EN-RAGE N-terminal amino acid sequence SEQ ID NO:2.
XX

KW Bovine; EN-RAGE; extracellular novel RAGE binding protein;
KW receptor for advanced glycation endproduct; inflammation; inhibition;
KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;
KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;
KW autoimmune disorder; inflammatory disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 47
FT /note= "unspecified"
XX
PN WO200020621-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-US023303.
XX
PR 06-OCT-1998; 98US-00167705.
PR 05-MAR-1999; 99US-00263312.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Schmidt AM, Stern D;
XX
DR WPI; 2000-303794/26.
XX
PT New human EN-RAGE (extracellular novel receptor for advanced glycation
PT end products) peptide, useful for identifying anti-inflammatory compounds
PT that inhibit its interaction with RAGE.
XX
PS Claim 2; Page 41; 132pp; English.
XX
CC The present invention describes an isolated human EN-RAGE (extracellular
CC novel receptor for advanced glycation end products) peptide (PI). The EN-
CC RAGE peptide binds to RAGE which is a member of the immunoglobulin
CC superfamily of cell-surface molecules. A compound capable of inhibiting
CC the interaction of EN-RAGE with RAGE is useful for the suppression of
CC inflammation resulting from systemic lupus erythematosus, inflammatory
CC lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
CC inflammatory disorder in which the recruitment of EN-RAGE containing
CC inflammatory cells occurs. The compound is also useful for the treatment
CC of systemic lupus erythematosus, inflammatory lupus nephritis in a
CC subject. The human EN-RAGE peptide is useful for identifying compounds
CC that inhibit its interaction with RAGE. The present sequence represents
CC the specifically claimed human EN-RAGE N-terminal amino acid sequence
XX
SQ Sequence 50 AA;

Alignment Scores:
Pred. No.: 5.03e-06 Length: 50
Score: 15.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.30% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x AAY90763 (1-50)

QY 46 CACCAGTACTCCGTTCCGGTGGGGCATTTCCGACACCCCTCAACAAG 90
DB 15 HisGlnTyrSerValArgValGlyHisPheAspThrLeuAsnLys 29

RESULT 9
ABB43183
ID ABB43183 standard; peptide; 46 AA.
XX
AC ABB43183;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #10689 encoded by human foetal liver single exon probe.
XX

KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 35818; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 46 AA;

Alignment Scores:
Pred. No.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x ABB43183 (1-46)

QY 37 AACATCTTCCACCACTACTCCGTTCCG 63
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 10
AAM37021
ID AAM37021 standard; protein; 46 AA.
XX
AC AAM37021;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #11058 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX

PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 37290; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP;
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 46 AA;

Alignment Scores:
Pred. No.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x AAM37021 (1-46)

QY 37 AACATCTTCCACCACTACTCCGTTCCG 63
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 11
ABB26281
ID ABB26281 standard; protein; 46 AA.
XX
AC ABB26281;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #8280 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PT WPI; 2001-488899/53.
XX DR Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PT Claim 15; SEQ ID NO 28051; 530pp; English.
XX PS The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 46 AA;

Alignment Scores:
Pred. NO.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x ABB26281 (1-46)

QY 37 AACATCTTCCACCAGTACTCCGTTCCG 63
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 12
AAM76914
ID AAM76914 standard; protein; 46 AA.
XX AAM76914;
AC
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37220.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000668.
XX PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX Example 4; SEQ ID NO 37220; 658pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX SQ Sequence 46 AA;

Alignment Scores:
Pred. NO.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x AAM76914 (1-46)

QY 37 AACATCTTCCACCAGTACTCCGTTCCG 63
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 13
AAM64093
ID AAM64093 standard; protein; 46 AA.
XX AAM64093;
AC
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36198.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000667.
XX PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX Example 4; SEQ ID NO 36198; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention

XX
SQ Sequence 46 AA;

Alignment Scores:
Pred. No.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x AAM64093 (1-46)

Qy 37 AACATCTTCCACCAGTACTCCGTTCCG 63
|||||
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 14
ABG58579
ID ABG58579 standard; peptide; 46 AA.
XX
AC ABG58579;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 37227.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
KW
XX Homo sapiens.
OS
XX WO200157273-A2.
PN
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488898/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
PT
XX Claim 27; SEQ ID NO 37227; 658pp; English.
PS
XX The invention relates to a single exon nucleic acid probe (SEN) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence

CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 46 AA;

Alignment Scores:
Pred. No.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x ABG58579 (1-46)

Qy 37 AACATCTTCCACCAGTACTCCGTTCCG 63
|||||
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 15
ABG46027
ID ABG46027 standard; peptide; 46 AA.
XX
AC ABG46027;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35692.

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2002-114183/15.
DR
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
PT
XX Claim 27; SEQ ID NO 35692; 634pp; English.
PS
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes

CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagenier syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 46 AA;

Alignment Scores:
Pred. No.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 5 Gaps: 0

US-09-910-208B-1 (1-276) x ABG46027 (1-46)

QY 37 AACATCTTCCACCAGTACTCCGTTCCG 63
Db 13 AsnilePheHisGlnTyrSerValArg 21

Search completed: February 23, 2005, 11:44:12
Job time : 133.5 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:45:12 ; Search time 88.5 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 115	7	7.6	327	17	US-10-923-960-21	Sequence 21, Appl	188	7	7.6	669	14	US-10-414-637-16	Sequence 16, Appl
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121	7	7.6	349	15	US-10-389-566-2148	Sequence 2148, Ap	194	7	7.6	670	14	US-10-414-637-44	Sequence 44, Appl
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C 123	7	7.6	362	17	US-10-923-960-25	Sequence 25, Appl	196	7	7.6	673	13	US-10-032-717-12	Sequence 12, Appl
C 124	7	7.6	368	16	US-10-437-963-135945	Sequence 135945,	197	7	7.6	673	13	US-10-032-717-18	Sequence 18, Appl
125	7	7.6	376	9	US-09-801-368-206	Sequence 206, App	198	7	7.6	673	13	US-10-032-717-22	Sequence 22, Appl
126	7	7.6	387	15	US-10-335-977-5987	Sequence 5987, Ap	199	7	7.6	673	13	US-10-032-717-40	Sequence 40, Appl
C 127	7	7.6	389	15	US-10-335-977-5988	Sequence 5988, Ap	200	7	7.6	673	14	US-10-414-637-12	Sequence 12, Appl
C 128	7	7.6	395	16	US-10-437-963-135896	Sequence 135896,	201	7	7.6	673	14	US-10-414-637-18	Sequence 18, Appl
129	7	7.6	401	16	US-10-437-963-152476	Sequence 152476,	202	7	7.6	673	14	US-10-414-637-22	Sequence 22, Appl
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C 136	7	7.6	434	17	US-10-919-272-70	Sequence 70, Appl	209	7	7.6	673	15	US-10-606-320-34	Sequence 34, Appl
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C 500 6 6.5

Sequence 486, App US-10-283-722-486 14 10
Sequence 506, App US-10-283-722-506 14 10
Sequence 610, App US-10-283-722-610 14 10
Sequence 613, App US-10-283-722-613 14 10
Sequence 173, App US-10-283-903-173 15 10
Sequence 280, App US-10-283-903-280 15 10
Sequence 310, App US-10-283-903-310 15 10
Sequence 486, App US-10-283-903-486 15 10
Sequence 506, App US-10-283-903-506 15 10
Sequence 610, App US-10-283-903-610 15 10
Sequence 613, App US-10-283-903-613 15 10
Sequence 40, Appl US-10-687-046-40 16 10
Sequence 229, App US-10-398-104-229 11 15
Sequence 54, Appl US-10-469-060-54 12 16
Sequence 1926, App US-10-468-496-1926 16 16
Sequence 1927, App US-10-468-496-1927 16 16
Sequence 2000, App US-10-468-496-2000 16 16
Sequence 2001, App US-10-468-496-2001 16 16
Sequence 267, App US-10-393-815-267 14 15
Sequence 141, App US-10-308-128-141 15 14
Sequence 50, Appl US-09-894-594-50 15 10
Sequence 3, Appli US-10-072-159-3 15 13
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Sequence 117, App US-10-378-173-117 16 15
Sequence 116, App US-10-378-173-116 17 15
Sequence 98, Appl US-10-432-465-98 20 15
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Sequence 67, Appl US-10-433-091-67 20 16
Sequence 68, Appl US-10-433-091-68 20 16
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Sequence 297, App US-10-372-876-297 23 15
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Sequence 748, App US-10-283-903-748 24 15
Sequence 38, Appl US-10-327-213-38 25 16
Sequence 97, Appl US-10-351-641-97 28 14
Sequence 47417, A US-09-864-761-47417 31 9
Sequence 39265, A US-09-864-761-39265 33 9
Sequence 61, Appl US-10-081-816-61 33 14
Sequence 231104, US-10-424-599-231104 36 15
Sequence 170, App US-09-726-643-170 37 9
Sequence 170, App US-10-042-141-170 37 13
Sequence 170, App US-10-919-272-170 37 17
Sequence 171028, US-10-437-963-171028 38 16
Sequence 58, Appl US-10-751-699-58 38 16
Sequence 43744, A US-09-864-761-43744 40 9
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Sequence 188401, US-10-424-599-188401 42 15
Sequence 232741, US-10-424-599-232741 43 15
Sequence 241587, US-10-424-599-241587 43 15
Sequence 41096, A US-09-864-761-41096 44 9
Sequence 27992, A US-10-029-386-27992 44 14
Sequence 196171, US-10-424-599-196171 44 15
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Sequence 39435, A US-09-864-761-39435 45 9
Sequence 185880, US-10-424-599-185880 46 15
Sequence 239332, US-10-424-599-239332 46 15
Sequence 268412, US-10-424-599-268412 46 15
Sequence 275687, US-10-424-599-275687 46 15
Sequence 108229, US-10-437-963-108229 46 16

ALIGNMENTS

RESULT 1
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. US20020106726A1

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; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Alignment Scores:
Pred. No.:      2.21e-77      Length: 90
Score:          90.00        Matches: 90
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    97.83%       Indels: 0
DB:             9           Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-3 (1-90)

QY      4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY      64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
      21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY      124 CCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGACCTG 183
      41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY      184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCCAGGGTG 243
      61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY      244 CTGAAAACAGCCCATAGATATCCACAAA 273
      81 LeuLysThrAlaHisIleAspIleHisLys 90

Db      81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 2
US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-4

Alignment Scores:
Pred. No.:      2.21e-77      Length: 90
Score:          90.00        Matches: 90
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    97.83%       Indels: 0
DB:             9           Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-4 (1-90)

QY      4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY      64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
      21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY      124 CCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGACCTG 183
      41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY      184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCCAGGGTG 243
      61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY      244 CTGAAAACAGCCCATAGATATCCACAAA 273
      81 LeuLysThrAlaHisIleAspIleHisLys 90

Db      81 LeuLysThrAlaHisIleAspIleHisLys 90

US-09-910-208B-1 (1-276) x US-09-872-185B-11 (1-90)
; Sequence 11, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-11

Alignment Scores:
Pred. No.:      2.21e-77      Length: 90
Score:          90.00        Matches: 90
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    97.83%       Indels: 0
DB:             9           Gaps: 0

US-09-910-208B-1 (1-276) x US-09-872-185B-11 (1-90)

QY      4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY      64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
      21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY      124 CCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGACCTG 183
      41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY      184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCCAGGGTG 243
      61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY      244 CTGAAAACAGCCCATAGATATCCACAAA 273
      81 LeuLysThrAlaHisIleAspIleHisLys 90

Db      81 LeuLysThrAlaHisIleAspIleHisLys 90
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QY      4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY      64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
      21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY      124 CCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGACCTG 183
      41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY      184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCCAGGGTG 243
      61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY      244 CTGAAAACAGCCCATAGATATCCACAAA 273
      81 LeuLysThrAlaHisIleAspIleHisLys 90

Db      81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 3
US-09-872-185B-11
; Sequence 11, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-11

Alignment Scores:
Pred. No.:      2.21e-77      Length: 90
Score:          90.00        Matches: 90
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    97.83%       Indels: 0
DB:             9           Gaps: 0

US-09-910-208B-1 (1-276) x US-09-872-185B-11 (1-90)

QY      4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
      1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY      64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAC 123
      21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY      124 CCCAAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGACCTG 183
      41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY      184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCCAGGGTG 243
      61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY      244 CTGAAAACAGCCCATAGATATCCACAAA 273
      81 LeuLysThrAlaHisIleAspIleHisLys 90

Db      81 LeuLysThrAlaHisIleAspIleHisLys 90
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RESULT 4

US-09-872-185B-12
; Sequence 12, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-12

Alignment Scores:
Pred. No.: 2.21e-77 Length: 90
Score: 90.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.83% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-872-185B-12 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGAGGGAATCATCAACATCTTCCACAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCGAAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGTGTCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAACACAGCCCATAGATATCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 5

US-10-666-513-3
; Sequence 3, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. US20040043412A1 RAGE Binding Protein (EN-RAGE)
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Human
US-10-666-513-3

Alignment Scores:

Pred. No.: 2.21e-77 Length: 90
Score: 90.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.83% Indels: 0
DB: 15 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-666-513-3 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGAGGGAATCATCAACATCTTCCACAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCGAAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGTGTCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAACACAGCCCATAGATATCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 6

US-10-665-867-3
; Sequence 3, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-3

Alignment Scores:

Pred. No.: 2.21e-77 Length: 90
Score: 90.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.83% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-665-867-3 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGAGGGAATCATCAACATCTTCCACAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCGAAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60


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; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-10-666-513-4

Alignment Scores:
Pred. No.:      2.75e-08      Length: 18
Score:          18.00        Matches: 18
Percent Similarity: 100.00%  Conservaive: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    19.57%      Indels: 0
DB:             15         Gaps: 0

US-09-910-208B-1 (1-276) x US-10-666-513-4 (1-18)
QY 196 GACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCACGGTGCTGAAA 249
    |||||||
Db 1 AspGlyAlaValSerPheGluGluPheValValLeuValSerArgValLeuLys 18

RESULT 11
US-10-665-867-5
; Sequence 5, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-10-665-867-5

Alignment Scores:
Pred. No.:      2.75e-08      Length: 18
Score:          18.00        Matches: 18
Percent Similarity: 100.00%  Conservaive: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    19.57%      Indels: 0
DB:             16         Gaps: 0

US-09-910-208B-1 (1-276) x US-10-665-867-5 (1-18)
QY 196 GACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGGTGTCACGGTGCTGAAA 249
    |||||||
Db 1 AspGlyAlaValSerPheGluGluPheValValLeuValSerArgValLeuLys 18

RESULT 12
US-09-826-589-2
; Sequence 2, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
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; LOCATION: (47)..(47)
; OTHER INFORMATION: x=any amino acid
US-09-826-589-2

Alignment Scores:
Pred. No.:      1.79e-05      Length: 50
Score:          15.00        Matches: 15
Percent Similarity: 100.00%  Conservaive: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    16.30%      Indels: 0
DB:             9         Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-2 (1-50)
QY 46 CACCAGTACTCCGTTCCGGTGGGGCATTTCGACACCCCTCAACAAG 90
    |||||||
Db 15 HisGlnTySerValArgValGlyHisPheAspThrLeuAsnLys 29

RESULT 13
US-09-872-185B-9
; Sequence 9, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Bovine
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (47)..(47)
; OTHER INFORMATION: Where Xaa = unknown
US-09-872-185B-9

Alignment Scores:
Pred. No.:      1.79e-05      Length: 50
Score:          15.00        Matches: 15
Percent Similarity: 100.00%  Conservaive: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    16.30%      Indels: 0
DB:             9         Gaps: 0

US-09-910-208B-1 (1-276) x US-09-872-185B-9 (1-50)
QY 46 CACCAGTACTCCGTTCCGGTGGGGCATTTCGACACCCCTCAACAAG 90
    |||||||
Db 15 HisGlnTySerValArgValGlyHisPheAspThrLeuAsnLys 29

RESULT 14
US-10-666-513-2
; Sequence 2, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. US20040043412a1e1 RAGE Binding Protein (EN-RAGE)
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (47)
; OTHER INFORMATION: Xaa at this position is unknown
US-10-666-513-2

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Pred. No.:      1.79e-05      Length:      50
Score:          15.00        Matches:      15
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    16.30%        Indels:      0
DB:             15           Gaps:         0

US-09-910-208B-1 (1-276) x US-10-666-513-2 (1-50)

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Db      15  HisGlnTyrSerValArgValGlyHisPheAspThrLeuAsnLys 29
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; Sequence 2, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50
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; NAME/KEY: MISC_FEATURE
; LOCATION: (47):(47)
; OTHER INFORMATION: x=any amino acid
US-10-665-867-2
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Alignment Scores:
Pred. No.:      1.79e-05      Length:      50
Score:          15.00        Matches:      15
Percent Similarity: 100.00%    Conservative: 0
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Db      15  HisGlnTyrSerValArgValGlyHisPheAspThrLeuAsnLys 29
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Search completed: February 23, 2005, 12:05:09
Job time : 94.5 secs

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ALIGNMENTS

RESULT 1
US-08-568-310D-19
; Sequence 19, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-19

Alignment Scores:
Pred. No.: 2.01e-82 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 2
US-09-270-455-19
Sequence 19, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19:
FROM 1 TO 92
US-09-270-455-19

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Pred. No.: 2.01e-82 Length: 92
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Query Match: 100.00% Indels: 0
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US-09-910-208B-1 (1-276) x US-09-270-455-19 (1-92)

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RESULT 3
US-09-263-312-3
Sequence 3, Application US/09263312
Patent No. 6555340

; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. 6555340e1 RAGE Binding Protein (EN-RAGE) and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/55873-A
; CURRENT APPLICATION NUMBER: US/09/263,312
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Human
US-09-263-312-3

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Pred. No.: 1.89e-80 Length: 90
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.83% Indels: 0
DB: 4 Gaps: 0

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RESULT 4
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; Sequence 3, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Alignment Scores:
Pred. No.: 1.89e-80 Length: 90
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Best Local Similarity: 100.00% Mismatches: 0
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RESULT 4
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Alignment Scores:
Pred. No.: 1.89e-80 Length: 90
Score: 90.00 Matches: 90
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.83% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-3 (1-90)

US-09-910-208B-1 (1-276) x US-09-826-589-3 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAGTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAAACCTCCAGAACACCAAGATCAACCTTACCATTCGAGGAATTCGTAGTCTCCTGGTGCCAGGGTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCCTGGTGCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

RESULT 5
US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-4

Alignment Scores:
Pred. No.: 1.89e-80 Length: 90
Score: 90.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.83% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-4 (1-90)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAAGTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAAACCTCCAGAACACCAAGATCAACCTTACCATTCGAGGAATTCGTAGTCTCCTGGTGCCAGGGTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCCTGGTGCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

RESULT 6
US-08-568-310D-2

; Sequence 2, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 2:
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51
US-08-568-310D-2

Alignment Scores:
Pred. No.: 5.72e-42 Length: 51
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.43% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-2 (1-51)

Qy 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
Qy 64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACCT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
Qy 124 CCCAAAACCTCCAGAACACCAAGATCAACCT 156
Db 41 ProlysThrLeuGlnAsnThrLysAspGlnPro 51

RESULT 7
US-09-270-455-2
; Sequence 2, Application US/09270455

; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,455
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/568,310
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51
US-09-270-455-2

Alignment Scores:
Pred. No.: 5.72e-42 Length: 51
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.43% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-2 (1-51)

Qy 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
Qy 64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACCT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
Qy 124 CCCAAAACCTCCAGAACACCAAGATCAACCT 156
Db 41 ProlysThrLeuGlnAsnThrLysAspGlnPro 51

RESULT 8
US-08-568-310D-6
; Sequence 6, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:

APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 31
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 6:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 31
US-08-568-310D-6
Alignment Scores:
Pred. No.: 3.17e-22 Length: 31
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.70% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-1 (1-276) x US-08-568-310D-6 (1-31)
QY 121 CTTCCCAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 1 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 20
QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTT 213
Db 21 LeuAspAlaAspLysAspGlyAlaValSerPhe 31
RESULT 9
US-09-270-455-6
Sequence 6, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 31
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 TO 31
US-09-270-455-6
Alignment Scores:
Pred. No.: 3.17e-22 Length: 31
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.70% Indels: 0
DB: 3 Gaps: 0
US-09-910-208B-1 (1-276) x US-09-270-455-6 (1-31)
QY 121 CTTCCCAAACCCCTCCAGAACACCAAGATCAACCTACCATTGACAAAATATTCCAAGAC 180
Db 1 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 20
QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTT 213
Db 21 LeuAspAlaAspLysAspGlyAlaValSerPhe 31
RESULT 10
US-08-568-310D-7
Sequence 7, Application US/08568310D
Patent No. 5976832
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY

STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 40
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 7:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 20

US-08-568-310D-7

Alignment Scores:
Pred. No.: 2.33e-11 Length: 20
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-7 (1-20)

Qy 217 GAATTCGTAGTCTGGTGTCCAGGGTGCTGAAACAGCCACATAGATATCCACAAAGAG 276
|||||
Db 1 GluPheValValLeuValSerArgValLeuLysThrAlaHisIleAspIleHisLysGlu 20

RESULT 11

US-09-270-455-7
Sequence 7, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 20

US-09-270-455-7

Alignment Scores:
Pred. No.: 2.33e-11 Length: 20
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-7 (1-20)

Qy 217 GAATTCGTAGTCTGGTGTCCAGGGTGCTGAAACAGCCACATAGATATCCACAAAGAG 276
|||||
Db 1 GluPheValValLeuValSerArgValLeuLysThrAlaHisIleAspIleHisLysGlu 20

RESULT 12

US-08-794-000-2
Sequence 2, Application US/08794000
Patent No. 6087123
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Metal-Containing Ribonucleotide Polypeptides
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,000
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE96/01337
FILING DATE: 17-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 25 992.0
FILING DATE: 17-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 30 500.0
FILING DATE: 18-AUG-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-794-000-2
Alignment Scores:


```
Pred. No.: 1.98e-11 Length: 91
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-794-000-2 (1-91)

Qy 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

RESULT 13
US-09-646-651C-1
; Sequence 1, Application US/09646651C
; Patent No. 6770455
; GENERAL INFORMATION:
; APPLICANT: Kieseewetter, Stefan
; APPLICANT: Kuhn, Eckehard
; APPLICANT: Koch-Pelster, Brigitte
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
; FILE REFERENCE: 206579
; CURRENT APPLICATION NUMBER: US/09/646,651C
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/EP98/07722
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: DE 198 11 047.2
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: Angiotropin-related protein
US-09-646-651C-1

Alignment Scores:
Pred. No.: 1.98e-11 Length: 91
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-646-651C-1 (1-91)

Qy 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

RESULT 14
US-09-263-312-4
; Sequence 4, Application US/09263312
; Patent No. 6555340
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. 6555340el RAGE Binding Protein (EN-RAGE) and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/55873-A
; CURRENT APPLICATION NUMBER: US/09/263,312
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
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; ORGANISM: Human
US-09-263-312-4

Alignment Scores:
Pred. No.: 2.21e-09 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.57% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-263-312-4 (1-18)

Qy 196 GACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGGTGTCAGGGTGCTGAAA 249
Db 1 AspGlyAlaValSerPheGluGluPheValValLeuValSerArgValLeuLys 18

RESULT 15
US-09-826-589-5
; Sequence 5, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-09-826-589-5

Alignment Scores:
Pred. No.: 2.21e-09 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.57% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-5 (1-18)

Qy 196 GACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGGTGTCAGGGTGCTGAAA 249
Db 1 AspGlyAlaValSerPheGluGluPheValValLeuValSerArgValLeuLys 18
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Search completed: February 23, 2005, 11:50:02
Job time : 36 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:01:38 ; Search time 27 Seconds
(without alignments)
1967.098 Million cell updates/sec

Title: US-09-910-208B-12
Perfect score: 477
Sequence: 1 atgacaaaacttgaagagca.....attaccacaccacaaaagag 276

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool_p/HADDAD-09-910208B/runat_23022005_101934_15302/app_query.fasta_1
-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208B @CGN 1 1 63 @runat_23022005_101934_15302 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	98.1	92	JC4712	S-100 calcium-bind
2	332	69.6	91	A55406	calgranulin c - pi
3	226.5	47.5	122	A42628	calgranulin B - bo
4	214.5	45.0	114	B31848	calgranulin B [val
5	194	40.7	95	S24146	S-100 protein P -
6	190	39.8	92	A48015	S-100 protein beta
7	189	39.6	92	BCHUIB	S-100 protein beta
8	187	39.2	92	A26557	S-100 protein beta
9	185	38.8	91	BCBOIB	S-100 protein beta
10	180.5	37.8	113	JN0686	calgranulin B - ra
11	178.5	37.4	113	S68242	calgranulin B - mo
12	177.5	37.2	95	S35985	S-100 protein alph
13	169.5	35.5	101	S06207	calvasculin - mous
14	168	35.2	591	A45135	profilaggrin - hum

15	167	35.0	102	1	JQ1300	calgizzarin - rabb
16	166.5	34.9	101	2	S01759	calvasculin - rat
17	162.5	34.1	94	1	BCBOIA	S-100 protein alph
18	161.5	33.9	94	1	BCHUIA	S-100 protein alph
19	158	33.1	93	1	BCHUCF	calgranulin A [val
20	157.5	33.0	101	2	A48219	calvasculin - huma
21	157	32.9	105	1	I37080	calgizzarin - huma
22	156	32.7	306	2	A48118	major epidermal ca
23	154	32.3	89	1	I56163	calgranulin A - mo
24	153.5	32.2	98	2	A41988	S-100 calcium-bind
25	152.5	32.0	100	2	A53217	placental calcium-
26	149	31.2	89	1	JN0685	calgranulin A - ra
27	147.5	30.9	90	1	BCHUY	calcyclin - human
28	147.5	30.9	97	2	A30129	S-100 protein, lun
29	146	30.6	110	2	B48219	S-100 calcium-bind
30	144.5	30.3	217	2	JE0330	26-kDa Ca2+-bindin
31	142.5	29.9	89	2	A54314	calcyclin - mouse
32	142.5	29.9	90	1	S27011	calcyclin - rabbit
33	139.5	29.2	90	2	B28363	calcyclin - rat
34	139	29.1	99	2	S20342	calcium-binding pr
35	137.5	28.8	98	2	JC5064	S-100 calcium-bind
36	136	28.5	65	2	A41004	calgizzarin - chic
37	127.5	26.7	95	1	LUPG10	calpactin I light
38	127.5	26.7	97	1	JH0663	calpactin I light
39	127.5	26.7	97	2	JC1139	calpactin I light
40	127.5	26.7	97	2	B28489	calpactin I light
41	126.5	26.5	97	2	A28489	calpactin I light
42	124	26.0	79	1	KLBOI	calcium-binding pr
43	123.5	25.9	95	2	A31373	calpactin I light
44	122.5	25.7	79	1	KLPGI	calcium-binding pr
45	121.5	25.5	79	1	JN0246	calcium-binding pr

ALIGNMENTS

RESULT 1

JC4712

S-100 calcium-binding protein A12 - human

N;Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; cal-

utrophil protein

C;Species: Homo sapiens (man)

C;Date: 10-May-1996 #sequence revision 19-Jul-1996 #text_change 09-Jul-2004

C;Accession: JC4712; JC4717; JC4891; S56113; S56114

R;Yamamura, T.; Hitomi, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsukada,

Biochem. Biophys. Res. Commun. 221, 356-360, 1996

A;Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping.

A;Reference number: JC4712; MUID:96192053; PMID:8619860

A;Accession: JC4712

A;Molecule type: mRNA

A;Residues: 1-92 <YAM>

A;Cross-references: UNIPROT:P80511; DDBJ:D83657; NID:g1502284; PIDN:BAA12030.1; PID:g150

R;Marti, T.; Erttmann, K.D.; Gallin, M.Y.

Biochem. Biophys. Res. Commun. 221, 454-458, 1996

A;Title: Host-parasite interaction in human onchocerciasis: Identification and sequence

A;Reference number: JC4717; MUID:96192069; PMID:8619876

A;Accession: JC4717

A;Molecule type: protein

A;Residues: 2-92 <MAR>

A;Experimental source: Onchocerca volvulus infecting human tissue

R;Ilg, E.C.; Troxler, H.; Buerigisser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hunz,

Biochem. Biophys. Res. Commun. 225, 146-150, 1996

A;Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP, s

A;Reference number: JC4891; MUID:96332419; PMID:8769108

A;Accession: JC4891

A;Molecule type: protein

A;Residues: 2-92 <ILG>

R;Guignard, F.; Mael, J.; Markert, M.

Biochem. J. 309, 395-401, (1995)

A;Title: Identification and Characterization of a novel human neutrophil protein relate

A;Reference number: S56113; MUID:95351965; PMID:7626002

A;Accession: S56113

A;Status: preliminary

A;Molecule type: protein

A;Residues: 'XX',4-14,'X',16-17,'XXXX' <GUI1>
A;Experimental source: isoform 6a
A;Accession: S56114
A;Status: preliminary
A;Molecule type: protein
A;Residues: 2-21 <GUI2>
A;Experimental source: isoform 6b
C;Comment: This protein is released by activated neutrophils in the course of inflammation
C;Genetics:
A;Gene: GDB:S100A12; p6; MRP6; CGRP; CAAF1
A;Cross-references: GDB:S218374
A;Map position: 1q21-1q21
C;Complex: monomer
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
F;2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAT>
F;6-39/Domain: calmodulin repeat homology <EF1>
F;49-81/Domain: calmodulin repeat homology <EF2>
F;86-90/Region: zinc binding #status predicted

Alignment Scores:
Pred. No.: 1.45e-43 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x JC4712 (1-92)
QY 1 ATGACAAAACCTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGCATTGTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
QY 121 CTGTCAAACACCATCAAGAATATCAAAGATAAAGCTGTCAATGATGAATATTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTAACACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 2
A55406
calgranulin c - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55406
R;Dell'Angelica, E.C.; Schleicher, C.H.; Santome, J.A.
J. Biol. Chem. 269, 28929-28936, 1994
A;Title: Primary structure and binding properties of calgranulin C, a novel S100-like ca
A;Reference number: A55406; MUID:95050708; PMID:7961855
A;Accession: A55406
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-91
A;Cross-references: UNIPROT:P80310
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand
F;48-80/Domain: calmodulin repeat homology <EF2>

Alignment Scores:
Pred. No.: 1.61e-28 Length: 91
Score: 332.00 Matches: 64
Percent Similarity: 81.32% Conservative: 10

Best Local Similarity: 70.33% Mismatches: 17
Query Match: 69.60% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-12 (1-276) x A55406 (1-91)
QY 4 ACAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTT 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTGTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAACACCATCAAGAATATCAAAGATAAAGCTGTCAATGATGAATATTCCAAGGCCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValLeuValThrAspVal 80
QY 244 CTGAAGGCTGCCCATTAACACACCCACAAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 3
A42628
calgranulin B - bovine (fragment)
N;Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory facto
in 2
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997
C;Accession: B22309; A42628
R;Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,
submitted to the Protein Sequence Database, July 1992
A;Reference number: A22309
A;Accession: B22309
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-122 <TAN>
R;Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.
Biochemistry 31, 5898-5905, 1992
A;Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophil
A;Reference number: A42628; MUID:92304974; PMID:1610833
A;Accession: A42628
A;Molecule type: protein
A;Residues: 4-32,'F',34-56 <DIA>
C;Complex: heterodimer and higher complexes with calgranulin A
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phos
F;6-40/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>

Alignment Scores:
Pred. No.: 7.74e-17 Length: 122
Score: 226.50 Matches: 47
Percent Similarity: 70.33% Conservative: 17
Best Local Similarity: 51.65% Mismatches: 26
Query Match: 47.48% Indels: 1
DB: 1 Gaps: 1

US-09-910-208B-12 (1-276) x A42628 (1-122)
QY 1 ATGACAAAACCTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetSerGlnMetGluSerSerIleGluThrIleIleAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGCATTGTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLeuGlyHisTyrAspThrLeuIleGlnLysGluSerLysGlnLeuValGlnLysGlu 40
QY 121 CTTGCAACACCATC---AAGATATCAAAGATAAAGCTGTTCATTGATGAATATTCCTCAA 177

Db 41 LeuProAsnPheLeuLysLysGlnLysLysAsnGluAlaAlaIleAsnGluIleMetGlu 60
QY 178 GGCCTGGATGCTAATCAAGATGAACAGGTCGACTTTCAGAATTTCATATCCCTGGTAGCC 237
Db 61 AspLeuAspThrAsnValAspLysGlnLeuSerPheGluGluPheIleMetLeuValAla 80
QY 238 ATTGGCTGAAGGCTGCCATTACCAACCCAC 270
Db 81 ArgLeuThrValAlaSerHisGluGluMethHis 91
RESULT 4
B31848
calgranulin B [validated] - human
N;Alternate names: calcium-binding protein MRP-14; cystic fibrosis-associated antigen (MRP-14); MIF-related 14K protein; S-100 calcium-binding protein A9 (S100A9)
C;Species: Homo sapiens (man)
C;Date: 21-May-1990 #sequence revision 23-May-1997 #text change 09-Jul-2004
C;Accession: B31848; S00667; A33819; B60911; B61082; D54327
R;Lagasse, E.; Clerc, R.G.
Mol. Cell. Biol. 8, 2402-2410, 1988
A;Title: Cloning and expression of two human genes encoding calcium-binding proteins the
A;Reference number: A93102; MUID:88302148; PMID:3405210
A;Accession: B31848
A;Molecule type: DNA
A;Residues: 1-114 <LAG>
A;Cross-references: UNIPROT:P06702; GB:M21064; NID:G188689; PIDN:AAA36326.1; PID:G386958
R;Odink, K.; Cerletti, N.; Brueggen, J.; Clerc, R.G.; Tarcsay, L.; Zwadlo, G.; Gerhards, Nature 330, 80-84, 1987
A;Title: Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis.
A;Reference number: S00667; MUID:88039099; PMID:3313057
A;Accession: S00667
A;Molecule type: mRNA
A;Residues: 1-114 <ODI>
A;Cross-references: EMBL:X06233; NID:G34770; PIDN:CAA29579.1; PID:G34771
A;Note: parts of this sequence were confirmed by protein sequencing
R;Murao, S.; Collart, F.R.; Huberman, E.
J. Biol. Chem. 264, 8356-8360, 1989
A;Title: A protein containing the cystic fibrosis antigen is an inhibitor of protein kin
A;Reference number: A33819; MUID:89255276; PMID:2656677
A;Accession: A33819
A;Molecule type: mRNA
A;Residues: 1-114 <MUR>
A;Cross-references: GB:M26311; NID:G862619; PIDN:AAA68480.1; PID:G516621
A;Note: part of this sequence was confirmed by protein sequencing; the amino end of the
R;Andersson, K.B.; Sletten, K.; Berntzen, H.B.; Dale, I.; Brandtzaeg, P.; Jellum, E.; Fa Scand. J. Immunol. 28, 241-245, 1988
A;Title: The leucocyte L1 protein: identity with the cystic fibrosis antigen and the cal
A;Reference number: A60911; MUID:88321575; PMID:3413449
A;Accession: B60911
A;Molecule type: protein
A;Residues: 39-42,'X',44-50;64-77,'X',79;84,'X',86-90,'X',92-94,'X',96-98 <AND>
R;Tobe, T.; Murakami, K.; Tomita, M.; Nozawa, R.
Chem. Pharm. Bull. 37, 1576-1580, 1989
A;Title: Amino acid sequences of 60B8 antigens induced in HL-60 cells by 1,25-dihydroxyv
A;Reference number: A61082; MUID:89376638; PMID:2776242
A;Accession: B61082
A;Molecule type: protein
A;Residues: 5-77;80-90,'A',92-114 <TOB>
A;Note: the blocked amino end of the mature protein is identified as 2-Thr; residue 91-H
R;Madsen, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Dejgaard, K.; Olsen, E.; Kiil, J E.
J. Invest. Dermatol. 97, 701-712, 1991
A;Title: Molecular cloning, occurrence, and expression of a novel partially secreted pro
A;Reference number: A54327; MUID:92043866; PMID:1940442
A;Accession: D54327
A;Molecule type: protein
A;Residues: 11-19;26-38;94-105,'X',107 <MAD>
A;Note: in several peptide samples no PTH was detected for 95-His but in one peptide PTH
C;Comment: This protein appears to be expressed only in cells of myeloid origin actively
C;Genetics: The presence of 3'-methylhistidine at position 105, corresponding to 107-His
A;Gene: GDB:S100A9; 60B8AG; CAGB; CFAG; LIAG; MAC387; MIF; MRP14; NIF; P14

A;Cross-references: GDB:120570; OMIM:123886
A;Map position: 1q21-1q21
A;Introns: 50/3
A;Note: the first intron occurs before the initiator codon
C;Complex: heterodimer and higher complexes with calgranulin A (see PIR:BCHUCF)
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; pho
F;2-114/Product: calgranulin B #status experimental <MAT>
F;10-44/Domain: calmodulin repeat homology <EF1>
F;54-86/Domain: calmodulin repeat homology <EF2>
F;2/Modified site: blocked amino end (Thr) (in mature form) (probably acetylated) #stat
F;113/Binding site: phosphate (Thr) (covalent) #status predicted
Alignment Scores:
Pred. No.: 1.64e-15 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 1 Gaps: 1
US-09-910-208B-12 (1-276) x B31848 (1-114)
QY 1 ATGACAAAACCTTGAGAGCATCTGGAGGGBATTGTCAATATCTTCCCAATACTCAGTT 60
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleIleAsnThrPheHisGlnTyrSerVal 24
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY 121 CTTGCAAAACACCATC---AAGAAATATCAAGATAAAGCTGTCTATTGATAATATTTCCAA 177
Db 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY 178 GGCCTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCC 237
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY 238 ATTGGCTGAAGGCTGCCATTACCAACCCACCAA 273
Db 85 ArgLeuThrTrpAlaSerHisGluLysMethHisGlu 96
RESULT 5
S24146
S-100 protein P - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S24146; PS0340
R;Becker, T.; Gerke, V.; Kube, E.; Weber, K.
Eur. J. Biochem. 207, 541-547, 1992
A;Title: S100P, a novel Ca(2+)-binding protein from human placenta. cDNA cloning, recom
A;Reference number: S24146; MUID:92339442; PMID:1633809
A;Accession: S24146
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-95 <BEC>
A;Cross-references: UNIPROT:P25815; EMBL:X65614; NID:G36177; PIDN:CAA46566.1; PID:G3617
R;Emoto, Y.; Kobayashi, R.; Akatsuka, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1246-1253, 1992
A;Title: Purification and characterization of a new member of the S-100 protein family
A;Reference number: PS0340; MUID:92171935; PMID:1540168
A;Accession: PS0340
A;Molecule type: protein
A;Residues: 1-31,'T',33-84,'X',86-91 <EMO>
A;Experimental source: placenta
C;Genetics:
A;Gene: GDB:S100P
A;Cross-references: GDB:134405; OMIM:600614
A;Map position: 4p16-4p16
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand; placenta
F;6-40/Domain: calmodulin repeat homology <EF1>


```
QY 190 AATCAAGATGAACAGGTCGACTTTCAGAA-----TTCATATCCCTGGTAGCCATT 240
|||::||| ::||| ||||| ||||| |||::||| ::|||::|
Db 65 AsnArgAspAsnGluValAspPheGlnGluTyrCysValPheLeuSerCysIleAlaMet 84
|||::||| ::||| ||||| ||||| |||::||| ::|||::|

QY 241 GCGCT-----GAAGGCTGCCATTACCACACCCACAAAGA 275
|||::||| ::||| ||||| ||||| |||::||| ::|||::|
Db 85 MetCysAsnGluPhePheGluGlyCysProAspLysGluProArgLys 100
|||::||| ::||| ||||| ||||| |||::||| ::|||::|

RESULT 14
A45135
profilaggrin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45135
R;Presland, R.B.; Haydock, P.V.; Fleckman, P.; Nirunsuksiri, W.; Dale, B.A.
J. Biol. Chem. 267, 23772-23781, 1992
A;Title: Characterization of the human epidermal profilaggrin gene. Genomic organization
A;Reference number: A45135; MUID:93054736; PMID:1429717
A;Accession: A45135
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-591 <PRE>
A;Cross-references: UNIPROT:Q01720; GB:L01089; GB:M90967; NID:G190408; PIDN:AAA60177.1;
A;Note: sequence extracted from NCBI backbone (NCBIP:118773)
C;Genetics:
A;Gene: GDB:FLG
A;Cross-references: GDB:119912; OMIM:135940
A;Map position: 1q21-1q21
C;Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology
C;Keywords: EF hand; epidermis; polymorphism; tandem repeat
F;49-81/Domain: calmodulin repeat homology <EF2>

Alignment Scores:
Pred. No.: 2.55e-10 Length: 591
Score: 168.00 Matches: 36
Percent Similarity: 60.87% Conservative: 20
Best Local Similarity: 39.13% Mismatches: 36
Query Match: 35.22% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x A45135 (1-591)

QY 1 ATGACAAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Db 1 MetSerThrLeuLeuGluAsnIlePheAlaIleIleAsnLeuPheLysGlnTyrSerLys 20
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||

QY 61 CGGAAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
|||::||| ::||| ||||| ||||| |||::||| ::|||::|
Db 21 LysAspLysAsnThrAspThrLeuSerLysLysGluLeuLysGluLeuGluLysGlu 40
|||::||| ::||| ||||| ||||| |||::||| ::|||::|

QY 121 CTTGCCAAACCATCAAGAATATCAAGATATAAGTGTCATTGATGAATATTTCCAAGGC 180
|||::||| ::||| ||||| ||||| |||::||| ::|||::|
Db 41 PheArgGlnIleLeuLysAsnProAspAspProAspMetValAspValPheMetAspHis 60
|||::||| ::||| ||||| ||||| |||::||| ::|||::|

QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTTCAAGAATTCATATCCCTGGTAGCCATT 240
|||::||| ::||| ||||| ||||| |||::||| ::|||::|
Db 61 LeuAspIleAspHisAsnLysLysIleAspPheThrGluPheLeuLeuMetValPheLys 80
|||::||| ::||| ||||| ||||| |||::||| ::|||::|

QY 241 GCGCTGAAGGCTGCCATTACCACACCCACAAAGAG 276
|||::||| ::||| ||||| ||||| |||::||| ::|||::|
Db 81 LeuAlaGlnAlaTyrTyrGluSerThrArgLysGlu 92
|||::||| ::||| ||||| ||||| |||::||| ::|||::|

RESULT 15
JQ1300
calgizzarin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ1300; PQ0243; B41004
R;Watanabe, M.; Ando, Y.; Todoroki, H.; Minami, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 181, 644-649, 1991
A;Title: Molecular cloning and sequencing of a cDNA clone encoding a new calcium binding
A;Reference number: JQ1300; MUID:92095968; PMID:1836726
```

```
A;Accession: JQ1300
A;Molecule type: mRNA
A;Residues: 1-102 <WAT>
A;Cross-references: UNIPROT:P24480; GB:D10586; GB:D90531; NID:G217745; PIDN:BAA01443.1;
A;Accession: PQ0243
A;Molecule type: protein
A;Residues: 25-49;53-62 <WAT2>
A;Experimental source: lung
R;Todoroki, H.; Kobayashi, R.; Watanabe, M.; Minami, H.; Hidaka, H.
J. Biol. Chem. 266, 18668-18673, 1991
A;Title: Purification, characterization, and partial sequence analysis of a newly identi
A;Reference number: A41004; MUID:92011625; PMID:1917990
A;Accession: B41004
A;Status: preliminary
A;Molecule type: protein
A;Residues: 25-49;53-58,'Y',60-62 <TOD>
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand
F;9-43/Domain: calmodulin repeat homology <EF1>
F;52-84/Domain: calmodulin repeat homology <EF2>

Alignment Scores:
Pred. No.: 2.93e-10 Length: 102
Score: 167.00 Matches: 34
Percent Similarity: 58.82% Conservative: 16
Best Local Similarity: 40.00% Mismatches: 35
Query Match: 35.01% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x JQ1300 (1-102)

QY 4 ACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCCG 63
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Db 5 ThrGluThrGluArgCysIleGluSerLeuIleAlaValPheGlnLysTyrAlaGlyLys 24
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||

QY 64 AAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Db 25 AspGlyHisSerValThrLeuSerLysThrGluPheLeuSerPheMetAsnThrGluLeu 44
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||

QY 124 GCAAACACCATCAAGAATATCAAGATATAAGCTGTTCATTGATGAATATTTCCAAGGCCTG 183
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Db 45 AlaAlaPheThrLysAsnGlnLysAspProGlyValLeuAspArgMetMetLysLysLeu 64
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||

QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Db 65 AspLeuAsnSerAspGlyGlnLeuAspPheGlnGluPheLeuAsnLeuIleGlyGlyLeu 84
|||::||| |||::||| |||::||| |||::||| |||::||| |||::|||

QY 244 CTGAAGGCTGCCCAT 258
|||::||| |||::||| |||::||| |||::||| |||::|||
Db 85 AlaValAlaCysHis 89
|||::||| |||::||| |||::||| |||::||| |||::|||

Search completed: February 23, 2005, 12:13:58
Job time : 29 secs
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:50:07 ; Search time 116.5 Seconds
(without alignments)
2426.332 Million cell updates/sec

Title: US-09-910-208B-12
Perfect score: 477
Sequence: 1 atgacaaaacttgaagagca.....attaccacaccacaaagag 276

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delopt 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO spool_p/HADDAD-09-910208B/runat 23022005 101933 15291/app_query.fasta_1
-DB=Uniprot_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208B @CGN 1 1 244 @runat 23022005 101933 15291 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463	97.1	91	1 S112 HUMAN	P80511 homo sapien
2	332	69.6	91	1 S112 PIG	P80310 sus scrofa
3	314	65.8	91	1 S112 BOVIN	P79105 bos taurus
4	273	57.2	81	1 S112 RABIT	O77791 oryctolagus
5	248	52.0	70	2 Q9TR16	Q9tr16 bos taurus
6	228.5	47.9	122	1 S109 BOVIN	P28783 bos taurus
7	218	45.7	119	2 Q6PRV2	Q6prv2 coturnix co
8	214.5	45.0	114	1 S109 HUMAN	P06702 homo sapien
9	210	44.0	119	1 M126_CHICK	P28318 gallus gall
10	201.5	42.2	118	1 S109_RABIT	P50117 oryctolagus
11	198	41.5	100	2 Q7ZVA4	Q7zva4 brachydanio
12	194	40.7	95	1 S10P HUMAN	P25815 homo sapien
13	190.5	39.9	99	2 Q8AYJ2	Q8ayj2 squalus aca
14	189	39.6	92	2 Q6YNR6	Q6ynr6 oryctolagus
15	189	39.6	92	2 Q925T3	Q925t3 cricetus
16	189	39.6	101	2 Q93395	Q93395 salvelinus

17	188	39.4	92	1 S101 ICTPU	Q91061 ictalurus p
18	186	39.0	92	2 Q9PSF6	Q9psf6 ictalurus p
19	185	38.8	91	1 S10B_BOVIN	P02638 bos taurus
20	185	38.8	91	1 S10B_MOUSE	P50114 mus musculu
21	184	38.6	91	1 S10B_HUMAN	P04271 homo sapien
22	183.5	38.5	95	2 Q6XG62	Q6xg62 brachydanio
23	182	38.2	91	1 S10B_RAT	P04631 rattus norv
24	180.5	37.8	111	2 Q761U7	Q761u7 rattus norv
25	180.5	37.8	112	1 S109_RAT	P50116 rattus norv
26	178.5	37.4	112	1 S109_MOUSE	P31725 mus musculu
27	177.5	37.2	95	1 S10A_MISFO	Q71zt1 misgurnus f
28	173.5	36.4	95	2 Q6DGT8	Q6dgt8 brachydanio
29	169.5	35.5	101	1 S104_MOUSE	P07091 mus musculu
30	169.5	35.5	102	2 Q68EI4	Q68ei4 brachydanio
31	168.5	35.3	98	1 S10Z_HUMAN	Q8wxg8 homo sapien
32	168	35.2	591	2 Q01720	Q01720 homo sapien
33	168	35.2	687	2 Q9H4U2	Q9h4u2 homo sapien
34	167	35.0	102	1 S111_RABIT	P24480 oryctolagus
35	166.5	34.9	101	1 S104_RAT	P05942 rattus norv
36	164.5	34.5	93	1 S10A_RAT	P35467 rattus norv
37	164	34.4	101	1 S111_CHICK	P24479 gallus gall
38	163	34.2	148	2 Q8BLX1	Q8blx1 mus musculu
39	163	34.2	2496	1 HORN_MOUSE	Q8vhd8 mus musculu
40	162.5	34.1	93	1 S10A_BOVIN	P02639 bos taurus
41	161.5	33.9	93	1 S10A_HUMAN	P23297 homo sapien
42	161.5	33.9	501	2 Q8CIU0	Q8ciu0 rattus norv
43	161	33.8	2850	1 HORN_HUMAN	Q86yz3 homo sapien
44	158	33.1	93	1 S108_HUMAN	P05109 h calgranul
45	158	33.1	1218	2 Q05331	Q05331 homo sapien

ALIGNMENTS

RESULT 1					
S112_HUMAN					
ID	S112_HUMAN	STANDARD;	PRT;	91 AA.	
AC	P80511; P83219;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Calgranulin C (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding protein in amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].				
GN	Name=S100A12;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1;				
RA	Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;				
RT	"Characterization of the human S100A12 (calgranulin C, p6, CAAF1, CGRP) gene, a new member of the S100 gene cluster on chromosome 1q21."				
RL	Cell Calcium 20:459-464 (1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96192053; PubMed=8619860; DOI=10.1006/bbrc.1996.0600;				
RA	Yamamura T., Hitomi J., Nagasaki K., Suzuki M., Takahashi E.;				
RA	Saito S., Tsukada T., Yamaguchi K.;				
RT	"Human CAAF1 gene -- molecular cloning, gene structure, and chromosome mapping."				
RL	Biochem. Biophys. Res. Commun. 221:356-360 (1996).				
RN	[3]				
RP	SEQUENCE.				
RX	MEDLINE=96192069; PubMed=8619876; DOI=10.1006/bbrc.1996.0616;				
RA	Marti T., Erttmann K.D., Gallin M.Y.;				
RT	"Host-parasite interaction in human onchocerciasis: identification and sequence analysis of a novel human calgranulin."				
RL	Biochem. Biophys. Res. Commun. 221:454-458 (1996).				
RN	[4]				
RP	SEQUENCE.				
RC	TISSUE=Neutrophils;				

RX MEDLINE=96332419; PubMed=8769108; DOI=10.1006/bbrc.1996.1144;
RA Ilg E.C., Troxler H., Buerigisser D.M., Kuster T., Markert M.,
RA Guignard F., Hunziker P., Birchler N., Heizmann C.W.;
RT "Amino acid sequence determination of human S100A12 (P6, calgranulin
C, CGRP, CAAF1) by tandem mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
RN [5]
RP SEQUENCE OF 1-20.
RX MEDLINE=95351965; PubMed=7626002;
RA Guignard F., Maue J., Markert M.;
RT "Identification and characterization of a novel human neutrophil
protein related to the S100 family.";
RL Biochem. J. 309:395-401(1995).
RN [6]
RP SEQUENCE OF 77-91, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY.
RC TISSUE=Nasal mucus;
RX MEDLINE=21413725; PubMed=11522286; DOI=10.1016/S0014-5793(01)02731-4;
RA Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;
RT "Calcitermin, a novel antimicrobial peptide isolated from human airway
secretions.";
RL FEBS Lett. 504:5-10(2001).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
RX MEDLINE=21065388; PubMed=11134923; DOI=10.1107/S090744490001458X;
RA Moroz O.V., Antson A.A., Murshudov G.N., Maitland N.J., Dodson G.G.,
RA Wilson K.S., Skibshoj I., Lukanidin E.M., Bronstein I.B.;
RT "The three-dimensional structure of human S100A12.";
RL Acta Crystallogr. D 57:20-29(2001).
CC -!- FUNCTION: Calcitermin possesses antifungal activity against
CC C.albicans and is also active against E.coli and P.aeruginosa but
CC not L.monocytogenes and S.aureus.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: Monocytes and lymphocytes.
CC -!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=1-91;
CC NOTE=Ref.6.
CC -!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=77-91;
CC NOTE=Ref.6.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
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CC -----
DR EMBL; X97859; CAA66453.1; -.
DR EMBL; X98288; CAA66934.1; -.
DR EMBL; X98289; CAA66934.1; JOINED.
DR EMBL; X98290; CAA66934.1; JOINED.
DR EMBL; X98289; CAB94792.1; -.
DR EMBL; X98290; CAB94792.1; JOINED.
DR EMBL; D49549; BAA08497.1; -.
DR EMBL; D83654; BAA12036.1; -.
DR EMBL; D83657; BAA12030.1; -.
DR PIR; JC4712; JC4712.
DR PDB; 1E8A; X-ray; A/B=1-91.
DR PDB; 1GQM; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-91.
DR PDB; 1ODB; X-ray; A/B/C/D/E/F=1-91.
DR Genew; HGNC:10489; S100A12.
DR MIM; 603112; -.
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0005626; C:insoluble fraction; TAS.
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001751; CaBP S100.
DR InterPro; IPR02048; EF-hand.
DR InterPro; IPR010983; EF Hand_like.
DR Pfam; PF00036; ehand; I.
DR Pfam; PF01023; S100; 1.
DR ProDom; PD003407; CaBP_S100; 1.

DR PROSITE; PS00018; EF HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW 3D-structure; Antibiotic; Calcium-binding; Direct protein sequencing;
FW Fungicide; Metal-binding; Zinc.
FT INIT MET 0 0 Calcitermin.
FT PEPTIDE 77 91 EF-hand 1; low affinity (By similarity).
FT CA_BIND 18 31 EF-hand 2; high affinity (By similarity).
FT CA_BIND 61 72
FT HELIX 2 18
FT TURN 19 19
FT TURN 24 25
FT STRAND 26 27
FT HELIX 29 39
FT TURN 41 43
FT TURN 45 48
FT HELIX 50 60
FT TURN 62 63
FT STRAND 68 69
FT HELIX 70 85
SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;

Alignment Scores:
Pred. No.: 5.54e-41 Length: 91
Score: 463.00 Matches: 91
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.06% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S112_HUMAN (1-91)
QY 4 ACAAACCTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 ThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGGCATTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGAGCTT 123
Db 21 LysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGluLeu 40
QY 124 GCAACACCATCAAGATATCAAGATAAAGCTGTCTATGATGAATATTCACAGGCCTG 183
Db 41 AlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60
QY 184 GATGCTATCAAGATGAACAGGTCGACTTTCAGAGATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80
QY 244 CTGAAGGTCGCCATTACCACACCCACAAAGAG 276
Db 81 LeuLysAlaAlaHisTyrHisThrHisLysGlu 91

RESULT 2
S112_PIG
ID S112_PIG STANDARD; PRT; 91 AA.
AC P80310;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC).
GN Name=S100A12;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC TISSUE=Granulocyte;
RX MEDLINE=95050708; PubMed=7961855;
RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
RT "Primary structure and binding properties of calgranulin C, a novel
S100-like calcium-binding protein from pig granulocytes.";
RL J. Biol. Chem. 269:28929-28936(1994).
CC -!- TISSUE SPECIFICITY: Found essentially in granulocytes with small


```
CC amounts found in lymphocytes.
CC -!- MISCELLANEOUS: In the absence of zinc binds one calcium ion per
CC molecule, in the presence of zinc binds two calcium ions per
CC molecule.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
DR PIR; A55406; A55406.
DR HSSP; P80511; 1E8A.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Direct protein sequencing; Metal-binding; Zinc.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 91 AA; 10614 MW; B4204461432D7FCE CRC64;

Alignment Scores:
Pred. No.: 7.22e-27 Length: 91
Score: 332.00 Matches: 64
Percent Similarity: 81.32% Conservative: 10
Best Local Similarity: 70.33% Mismatches: 17
Query Match: 69.60% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S112_PIG (1-91)

QY 4 ACAAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 AAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 GCAAAACCATCAAGAATATCAAGATAAAGCTGTGCTATTGATGAATATTTCCAAAGGCCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60

QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80

QY 244 CTGAAGGCTGCCCATTTACCACACCCCAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 3
S112_BOVIN STANDARD; PRT; 91 AA.
ID S112_BOVIN STANDARD; PRT; 91 AA.
AC P79105;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC) (Calcium-binding protein in amniotic fluid 1)
DE (CAAF1) (RAGE binding protein).
GN Name=S100A12; Synonyms=CAAF1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oesophagus;
RX MEDLINE=96298783; PubMed=8718672;
RA Hitomi J., Yamaguchi K., Kikuchi Y., Kimura T., Maruyama K.,
RA Nagasaki K.;
RT "A novel calcium-binding protein in amniotic fluid, CAAF1: its
```

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RT molecular cloning and tissue distribution.";
RL J. Cell Sci. 109:805-815(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=99325504; PubMed=10399917; DOI=10.1016/S0092-8674(00)80801-6;
RA Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C.,
RA Kambham N., Bierhaus A., Nawroth P., Neurath M.F., Slattey T.,
RA Beach D., McClary J., Nagashima M., Morser J., Stern D., Schmidt A.M.;
RT "RAGE mediates a novel proinflammatory axis: a central cell surface
RT receptor for S100/calgranulin polypeptides.";
RL Cell 97:889-901(1999).
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
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CC -----
CC EMBL; D49548; BAA08496.1; -.
CC EMBL; AF011757; AAB65423.1; -.
CC HSSP; P80511; 1GQM.
CC InterPro; IPR001751; CaBP_S100.
CC InterPro; IPR002048; EF-hand.
CC InterPro; IPR010983; EF_Hand_like.
CC Pfam; PF00036; ehand; 1.
CC Pfam; PF01023; S_100; 1.
CC ProDom; PD003407; CaBP_S100; 1.
CC PROSITE; PS00018; EF_HAND; 1.
CC PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Metal-binding; Zinc.
FT INIT_MET 0 0 By similarity.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

Alignment Scores:
Pred. No.: 6.28e-25 Length: 91
Score: 314.00 Matches: 60
Percent Similarity: 80.22% Conservative: 13
Best Local Similarity: 65.93% Mismatches: 18
Query Match: 65.83% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S112_BOVIN (1-91)

QY 4 ACAAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 AAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 GCAAAACCATCAAGAATATCAAGATAAAGCTGTGCTATTGATGAATATTTCCAAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAAGGCTGCCCATTTACCACACCCCAAGAG 276
Db 81 LeuLysThrAlaHisIleAspIleHisLysGlu 91

RESULT 4
S112_RABIT STANDARD; PRT; 81 AA.
ID S112_RABIT STANDARD; PRT; 81 AA.
```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88039099; PubMed=3313057; DOI=10.1038/330080a0;
RA Odink K., Cerletti N., Bruggen J., Clerc R.G., Tarcsay L., Zwaldo G.,
RA Gerhards G., Schlegel R., Sorg C.;
RT "Two calcium-binding proteins in infiltrate macrophages of rheumatoid
RT arthritis";
RL Nature 330:80-82(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88302148; PubMed=3405210;
RA Lagasse E., Clerc R.G.;
RA "Cloning and expression of two human genes encoding calcium-binding
RT proteins that are regulated during myeloid differentiation.";
RL Mol. Cell. Biol. 8:2402-2410(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89255276; PubMed=26566677;
RA Murao S., Collart F.R., Huberman E.;
RA "A protein containing the cystic fibrosis antigen is an inhibitor of
RT protein kinases";
RL J. Biol. Chem. 264:8356-8360(1989).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ARG-20.
RA Wang M., Xu X., Cai Y., Xu H., Han Y., Xu Z., Wu M.;
RA "Human gene for migration inhibitory factor-related protein 14
RT (MRP14), variant allele";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 84-114, AND PHOSPHORYLATION SITE THR-113.
RX MEDLINE=90044075; PubMed=2478889; DOI=10.1038/342189a0;
RA Edgeworth J., Freemont P., Hogg N.;
RA "Ionomycin-regulated phosphorylation of the myeloid calcium-binding
RT protein p14";
RL Nature 342:189-192(1989).
RN [7]
RP SEQUENCE OF 11-19; 26-37 AND 94-107.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [8]
RP SEQUENCE OF 5-34.

RX MEDLINE=93139333; PubMed=8423249;
RA Miyasaki K.T., Bodeau A.L., Murthy A.R., Lehrer R.I.;
RT "In vitro antimicrobial activity of the human neutrophil cytosolic S-
RL 100 protein complex, calprotectin, against Capnocytophaga sputigena.";
RL J. Dent. Res. 72:517-523(1993).
CC -!- FUNCTION: Expressed by macrophages in acutely inflamed tissues
CC and in chronic inflammations. Seen to be an inhibitor of protein
CC kinases. Also expressed in epithelial cells constitutively or
CC induced during dermatoses. May interact with components of the
CC intermediate filaments in monocytes and epithelial cells.
CC -!- MISCELLANEOUS: Has been shown to bind calcium.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X06233; CAA29579.1; -.
DR EMBL; M21064; AAA36326.1; -.
DR EMBL; M26311; AAA68480.1; -.
DR EMBL; AF237581; AAF62536.1; -.
DR EMBL; AF237582; AAF62537.1; -.
DR EMBL; A12029; CAA01002.1; -.
DR EMBL; A12032; CAA01004.1; -.
DR EMBL; BC047681; AAH47681.1; -.
DR PIR; B31848; B31848.
DR PDB; 1IRJ; X-ray; A/B/C/D/E/F/G/H=2-114.
DR SWISS-2DPAGE; P06702; HUMAN.
DR Aarhus/Ghent-2DPAGE; 5007; IEF.
DR Aarhus/Ghent-2DPAGE; 6010; IEF.
DR Aarhus/Ghent-2DPAGE; 6017; IEF.
DR Aarhus/Ghent-2DPAGE; 7013; IEF.
DR OGP; P06702; -.
DR PMMA-2DPAGE; P06702; -.
DR Genew; HGNC:10499; S100A9.
DR MIM; 123886; -.
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0004871; R:signal transducer activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW 3D-structure; Calcium-binding; Direct protein sequencing; Macrophage;
KW Phosphorylation; Polymorphism.
FT CA_BIND 23 36 EF-hand 1; low affinity (Potential).
FT CA_BIND 67 78 EF-hand 2; high affinity (Potential).
FT MOD_RES 113 113 Phosphothreonine.
FT VARIANT 20 20 H -> R.
FT CONFLICT 6 6 /FTid=VAR_013008.
FT CONFLICT 25 25 S -> H (in Ref. 8).
FT CONFLICT 28 28 K -> F (in Ref. 8).
FT HELIX 7 23 H -> L (in Ref. 8).
FT TURN 24 24
FT TURN 29 30
FT STRAND 32 32
FT HELIX 34 44
FT TURN 46 51
FT HELIX 52 54
FT HELIX 56 66
FT TURN 68 69
FT STRAND 74 74


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or send an email to license@isb-sib.ch).
-----
DR EMBL; AF091849; AAC61771.1; -.
DR EMBL; D17404; BAA04227.1; -.
DR PIR; I46861; I46861.
DR HSSP; P06702; 1IRJ.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF_HAND.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Repeat.
FT NON TER 1
FT CA_BIND 9 22 EF-hand 1; low affinity (Potential).
FT CA_BIND 53 64 EF-hand 2; high affinity (Potential).
FT DOMAIN 103 118 2 X 8 AA tandem repeats of G-H-G-H-G-H-S-
H.
FT REPEAT 103 110 1.
FT REPEAT 111 118 2.
FT SEQUENCE 118 AA; 13292 MW; 7496118E21AD5C41 CRC64;

Alignment Scores:
Pred. No.: 8.32e-13 Length: 118
Score: 201.50 Matches: 41
Percent Similarity: 70.73% Conservative: 17
Best Local Similarity: 50.00% Mismatches: 23
Query Match: 42.24% Indels: 1
DB: 1 Gaps: 1

US-09-910-208B-12 (1-276) x S109_RABIT (1-118)

QY 31 ATTGTCAATATCTTCACCAATACTCAGTTCGGAAGGGGCATTTTGACACCCCTCTCTAAG 90
Db 1 IleIleAsnIlePheHisGlnTyrSerValArgValGlyProArgAspSerLeuSerGln 20
QY 91 GGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTTGCAACACCATC---AAGAAATATCAA 147
Db 21 LysGluPheLysGlnLeuValGlnLysGluLeuHisAsnPheLeuLysLysGluAlaArg 40
QY 148 GATAAAGCTGTCAATTCATGAAATATTCACGGCCTGGATGCTAATCAAGATGAACAGGTC 207
Db 41 AspGluLysAlaIleAsnAspIleMetGluAspLeuAspThrAsnGlnAspLysGlnLeu 60
QY 208 GACTTTCAAGAATTCATATCCCTGGTAGCCATTCGGCTGAAGGCTGCCCATACACACC 267
Db 61 SerPheGluGluPheValIleLeuMetAlaArgLeuValHisAlaSerHisGluGluMet 80
QY 268 CACAAA 273
Db 81 HisLys 82

RESULT 11
Q7ZVA4
ID Q7ZVA4 PRELIMINARY; PRT; 100 AA.
AC Q7ZVA4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Zgc:56142.
GN ORFNames=zgc:56142;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
```

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OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; BC045941; AAH45941.1; -.
DR HSSP; P35467; 1K2H.
DR ZFIN; ZDB-GENE-040426-1937; zgc:56142.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 100 AA; 11157 MW; DAB81814E54CB8C8 CRC64;

Alignment Scores:
Pred. No.: 1.98e-12 Length: 100
Score: 198.00 Matches: 38
Percent Similarity: 76.00% Conservative: 19
Best Local Similarity: 50.67% Mismatches: 18
Query Match: 41.51% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x Q7ZVA4 (1-100)

QY 10 CTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCGGAAGSG 69
Db 5 LeuGluArgAlaMetGluThrLeuIleThrValPheHisArgTyrSerGlyAlaGluGly 24
QY 70 CATTTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGTACAAAGGAGCTTGCAAAC 129
Db 25 AsnSerSerThrLeuSerArgArgGluLeuLysGlnLeuMetGluLysGluLeuAlaSer 44
QY 130 ACCATCAAGAATATCAAAGATAAGCTGTCAATTGATGAATAATATCCAAGGCCTGATGCT 189
Db 45 PheLeuLysSerGlnLysAspProAlaAlaValAspLysIleMetLysAspLeuAspAla 64
QY 190 AATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGGTA 234
Db 65 AsnGlyAspGlyGluValAsnPheGluGluPheValSerLeuVal 79

RESULT 12
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S10P_HUMAN
ID S10P_HUMAN STANDARD; PRT; 95 AA.
AC P25815;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-100P protein.
GN Name=S100P; Synonyms=S100E;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92339442; PubMed=1633809;
RA Becker T., Gerke V., Kube E., Weber K.;
RT "S100P, a novel Ca(2+)-binding protein from human placenta. cDNA
cloning, recombinant protein expression and Ca2+ binding properties.";
RL Eur. J. Biochem. 207:541-547(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Jin G., Wang S., Chen J.;
RT "Cloning, expression and characterization of a novel human calcium-
binding S100 gene.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1-91.
RC TISSUE=Placenta;
RX MEDLINE=92171935; PubMed=1540168;
RA Emoto Y., Kobayashi R., Akatsuka H., Hidaka H.;
RT "Purification and characterization of a new member of the S-100
protein family from human placenta.";
RL Biochem. Biophys. Res. Commun. 182:1246-1253(1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX PubMed=12507480; DOI=10.1016/S0022-2836(02)01278-0;
RA Zhang H., Wang G., Ding Y., Wang Z., Barracough R., Rudland P.S.,
RA Fernig D.G., Rao Z.;
RT "The crystal structure at 2A resolution of the Ca2+ -binding protein
S100P.";
RL J. Mol. Biol. 325:785-794(2003).
CC -1- SUBUNIT: Homodimer. Interacts with S100Z.
CC -1- MISCELLANEOUS: This protein binds two calcium ions.
CC -1- SIMILARITY: Belongs to the S-100 family.
CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.

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CC -----
DR EMBL; X65614; CAA46566.1; --
DR EMBL; AF539739; AAO41114.1; --
DR EMBL; BC006819; AAH06819.1; --
DR PIR; S24146; S24146.
DR PDB; 1J55; X-ray; A=1-95.
DR Genew; HGNC:10504; S100P.
DR H-InvDB; HIX0004067; --
DR MIM; 600614; --
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0005515; F:protein binding; TAS.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW 3D-structure; Calcium-binding; Direct protein sequencing; Placenta.
FT CA_BIND 19 32 EF-hand 1; low affinity.
FT CA_BIND 62 73 EF-hand 2; high affinity.
FT CONFLICT 32 32 E -> T (in Ref. 4).
FT CONFLICT 44 44 F -> E (in Ref. 4).
FT HELIX 3 18
FT TURN 19 20
FT TURN 25 26
FT STRAND 27 28
FT HELIX 30 40
FT TURN 42 43
FT HELIX 53 61
FT STRAND 69 70
FT HELIX 71 92
FT TURN 93 93
SQ SEQUENCE 95 AA; 10400 MW; 786E6E3F3EACC6C1 CRC64;

Alignment Scores:
Pred. No.: 5,35e-12 Length: 95
Score: 194.00 Matches: 41
Percent Similarity: 63.74% Conservative: 17
Best Local Similarity: 45.05% Mismatches: 33
Query Match: 40.67% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S10P_HUMAN (1-95)

QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrGluLeuGluThrAlaMetGlyMetIleIleAspValPheSerArgTyrSerGly 20
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 SerGluGlySerThrGlnThrLeuThrLysGlyGluLeuLysValLeuMetGluLysGlu 40
QY 121 CTTGCAACACCATCAAGAATATCAAGATAAAGCTGTGATGATAATATTCCAAGGC 180
Db 41 LeuProGlyPheLeuGlnSerGlyLysAspLysAspAlaValAspLysLeuLeuLysAsp 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlyAspAlaGlnValAspPheSerGluPheIleValPheValAlaAla 80
QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAA 273
Db 81 IleThrSerAlaCysHisLysTyrPheGluLys 91

RESULT 13
Q8AYJ2


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ID Q8AYJ2 PRELIMINARY; PRT; 99 AA.
AC Q8AYJ2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-100 calcium-binding protein A1.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hynostomalea; Squaliformes; Squaloidei;
OC Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang C., Callard G.V.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; AF421551; AAN63527.1; -.
DR HSSP; P35467; IK2H.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 99 AA; 11050 MW; BA62D8190A4A3693 CRC64;

Alignment Scores:
Pred. No.: 1.27e-11 Length: 99
Score: 190.50 Matches: 40
Percent Similarity: 69.41% Conservative: 19
Best Local Similarity: 47.06% Mismatches: 25
Query Match: 39.94% Indels: 1
DB: 2

US-09-910-208B-12 (1-276) x Q8AYJ2 (1-99)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrGluLeuGluSerAlaMetAlaGlyIleGlyValPheArgLysTyrSerGly 20
QY 61 CGGAAGGGGCATTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 LysGluGlyAspLysTyrSerLeuSerAsnAsnGluMetValAspLeuLeuLysAlaGlu 40
QY 121 CTTCGAAACACCATCAAGAATATCAAGATATAAGCTGTGATGATGAAATATTCGAAGC 180
Db 41 LeuProAsnPheLeuLysSerGlnLysAspLysAlaAlaValAspLysIleMetLysAsp 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspArgAsnLysAspGlyGluLeuAspPheGlnGluPheValValLeuIleAla--- 79
QY 241 GCGCTGAAGGCTGCC 255
Db 80 AlaLeuAlaAlaAla 84

RESULT 14
Q6YNR6 PRELIMINARY; PRT; 92 AA.
AC Q6YNR6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE S-100 calcium-binding protein beta subunit.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC TISSUE=Cerebellum;
RA Qian Z., Barmack N.H.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; AY050568; AAL12231.1; -.
DR HSSP; P04631; 1B4C.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR SMART; SM00054; EFh; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 92 AA; 10713 MW; 43815AC212A3AD6B CRC64;

Alignment Scores:
Pred. No.: 1.85e-11 Length: 92
Score: 189.00 Matches: 34
Percent Similarity: 69.77% Conservative: 26
Best Local Similarity: 39.53% Mismatches: 26
Query Match: 39.62% Indels: 0
DB: 2

US-09-910-208B-12 (1-276) x Q6YNR6 (1-92)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetSerGluLeuGluLysAlaMetValAlaLeuIleAspValPheHisGlnTyrSerGly 20
QY 61 CGGAAGGGGCATTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgGluGlyAspLysHisLysLeuLysLysSerGluLeuLysGluLeuIleAsnAsnGlu 40
QY 121 CTTCGAAACACCATCAAGAATATCAAGATATAAGCTGTGATGATGAAATATTCGAAGC 180
Db 41 LeuSerHisPheLeuGluGluIleLysGluGlnValValAspLysValMetGluThr 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAsnAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValAlaMet 80
QY 241 GCGCTGAAGGCTGCCCAT 258
Db 81 ValThrThrAlaCysHis 86

RESULT 15
Q925T3 PRELIMINARY; PRT; 92 AA.
AC Q925T3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S100B.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuge O., Yamakawa Y., Nishijima M.;
RT "Enhancement of transport-dependent decarboxylation of
RT phosphatidylserine by S100B protein in permeabilized Chinese hamster
RT ovary cells."
RL J. Biol. Chem. 0:0-0(2001).
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; AB056121; BAB43945.1; -.
DR HSSP; P04631; 1B4C.
DR GO; GO:0005737; C:cytoplasm; ISS.
DR GO; GO:0005576; C:extracellular; ISS.
```

DR GO; GO:0005509; F:calcium ion binding; ISS.
DR GO; GO:0019210; F:kinase inhibitor activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; ISS.
DR GO; GO:0048155; F:S100 alpha binding; ISS.
DR GO; GO:0048154; F:S100 beta binding; ISS.
DR GO; GO:0048156; F:tau protein binding; ISS.
DR GO; GO:0008270; F:zinc ion binding; ISS.
DR GO; GO:0048143; P:astrocyte activation; ISS.
DR GO; GO:0007409; P:axonogenesis; ISS.
DR GO; GO:0006874; P:calcium ion homeostasis; ISS.
DR GO; GO:0006112; P:energy reserve metabolism; ISS.
DR GO; GO:0048151; P:hyperphosphorylation; ISS.
DR GO; GO:0006917; P:induction of apoptosis; ISS.
DR GO; GO:0007611; P:learning and/or memory; ISS.
DR GO; GO:0045917; P:positive regulation of complement activation; ISS.
DR GO; GO:0042035; P:regulation of cytokine biosynthesis; ISS.
DR GO; GO:0048169; P:regulation of long-term neuronal synaptic p. . .; ISS.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CaBP; 1.
SQ SEQUENCE 92 AA; 10749 MW; AF50107EC2BEDF6B CRC64;

Alignment Scores:
Pred. No.: 1.85e-11 Length: 92
Score: 189.00 Matches: 35
Percent Similarity: 67.39% Conservative: 27
Best Local Similarity: 38.04% Mismatches: 30
Query Match: 39.62% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x Q925T3 (1-92)

Qy	1	ATGACAAAAC	TTGAAGAGCATCTGGAGGAATTGCAATATCTTCCACCAATACTCAGTT	60
Db	1	MetSerGluLeuGluLysAlaMetValAlaLeuIleAspIlePheHisGlnTyrSerGly	20	
Qy	61	CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG	120	
Db	21	ArgGluGlyAspLysHisLysLeuLysLysSerGluLeuLysGluLeuIleAsnAsnGlu	40	
Qy	121	CTTGCAAAACCATCAAGAAATATCAAAGATAAAGCTGTGATTGATGAATATTCCAAGGC	180	
Db	41	LeuSerHisPheLeuGluGluIleLysGluGlnGluValValAspLysValMetGluThr	60	
Qy	181	CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATT	240	
Db	61	LeuAspGluAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValSerMet	80	
Qy	241	GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG	276	
Db	81	ValThrThrAlaCysHisGluPhePheGluGlnGlu	92	

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:49:17 ; Search time 114 Seconds
(without alignments)
1872.734 Million cell updates/sec

Title: US-09-910-208B-12
Perfect score: 477
Sequence: 1 atgacaaaacttgagagca.....attaccacaccacaaagag 276

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/HADDAD-09-910208B/runat_23022005_101933_15284/app_query.fasta_1
-DB=A Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208B @CGN_1_1_224 @runat_23022005_101933_15284 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	98.1	92	2 AAW03564	Aaw03564 Calcium b
2	468	98.1	92	2 AAW24137	Aaw24137 Human che
3	468	98.1	92	3 AAB45542	Aab45542 Human S10
4	468	98.1	92	4 AAB31911	Aab31911 Amino aci
5	468	98.1	92	4 AAB31907	Aab31907 Amino aci
6	468	98.1	92	4 AAB31908	Aab31908 Amino aci
7	468	98.1	92	7 ADA93649	Ada93649 Human cal
8	468	98.1	92	8 ADN04192	Adn04192 Antipsori
9	468	98.1	92	8 ADO19540	Ado19540 Human PRO
10	468	98.1	92	8 ADR14333	Adr14333 Human NF-

11	468	98.1	92	8 ADP23921	Adp23921 PRO polyp
12	468	98.1	92	8 ADS74331	Ads74331 PRO polyp
13	463	97.1	91	4 AAB31909	Aab31909 Amino aci
14	442	92.7	95	4 ABG27582	Abg27582 Novel hum
15	332	69.6	91	2 AAW01826	Aaw01826 Component
16	332	69.6	91	2 AAW93819	Aaw93819 Angiotrop
17	319	66.9	92	2 AAW03563	Aaw03563 Calcium b
18	309	64.8	90	3 AAY90765	Aay90765 Bovine CA
19	309	64.8	90	3 AAY90764	Aay90764 Bovine co
20	234	49.1	46	4 ABB43183	Abb43183 Peptide #
21	234	49.1	46	4 AAM37021	Aam37021 Peptide #
22	234	49.1	46	4 ABB26281	Abb26281 Protein #
23	234	49.1	46	4 AAM76914	Aam76914 Human bon
24	234	49.1	46	4 AAM64093	Aam64093 Human bra
25	234	49.1	46	4 ABG58579	Abg58579 Human liv
26	234	49.1	46	5 ABG46027	Abg46027 Human pep
27	224	47.0	363	4 ABG27581	Abg27581 Novel hum
28	214.5	45.0	114	2 AAW17062	Aaw17062 Human mul
29	214.5	45.0	114	2 AAW60178	Aaw60178 Human cal
30	214.5	45.0	114	2 AAY48615	Aay48615 Human bre
31	214.5	45.0	114	3 AAY87637	Aay87637 Human cal
32	214.5	45.0	114	3 AAB45539	Aab45539 Human S10
33	214.5	45.0	114	4 ABB44613	Abb44613 Human wou
34	214.5	45.0	114	4 AAB31905	Aab31905 Amino aci
35	214.5	45.0	114	6 ABB82712	Abb82712 Human MRP
36	214.5	45.0	114	7 ADB17567	Adb17567 Human mye
37	214.5	45.0	114	7 ADE57110	Ade57110 Human Pro
38	214.5	45.0	114	7 ADE34548	Ade34548 Human mig
39	214.5	45.0	114	7 ADF09358	Adf09358 Human cal
40	214.5	45.0	114	8 ADL83164	Adl83164 Human PRO
41	214.5	45.0	114	8 ADN03968	Adn03968 Antipsori
42	214.5	45.0	114	8 ADQ30562	Adq30562 Pancreas
43	214.5	45.0	114	8 ADR14329	Adr14329 Human NF-
44	214.5	45.0	114	8 ABM80144	Abm80144 Tumour-as
45	214.5	45.0	114	8 ADP23562	Adp23562 PRO polyp

ALIGNMENTS

RESULT 1
AAW03564

ID AAW03564 standard; protein; 92 AA.

XX

AC AAW03564;

XX 01-MAY-1997 (first entry)

DT Calcium binding protein CAAF1.

DE
KW Calcium binding protein; human; amniotic fluid; S100 protein family;
KW intracellular signal transduction; squamous epithelial cell; neutrophil;
KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW squamous cell carcinoma; skin; oesophagus; CAAF1; lung; blood disease.

XX Homo sapiens.

OS
XX EP731166-A2.

PD 11-SEP-1996.

XX 04-DEC-1995; 95EP-00119045.

PR 06-MAR-1995; 95JP-00045564.

PR 06-MAR-1995; 95JP-00070468.

XX (TOFU) TONEN CORP.

PA (HITO/) HITOMI J.

XX Hitomi J, Yamaguchi K, Yamamura T, Kimura T;

DR WPI; 1996-403989/41.

DR N-PSDB; AAT39346.

XX

PT New human or bovine calcium binding protein and related nucleic acid - is
PT a marker for inflammation, neoplasia, skin and blood diseases.

XX
PS Claim 1; Page 24; 36pp; English.

XX This sequence represents the CAAF1 calcium-binding protein isolated from
CC human amniotic fluid. CAAF1 belongs to the S100 protein family, which
CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion
CC concentration is one of the key factors for intracellular signal
CC transduction. The calcium signals are transduced by various calcium-
CC binding proteins, such as this protein. CAAF1 is normally expressed in
CC squamous epithelial cells, neutrophils and macrophages, but atypical
CC epithelial cells are negative for CAAF1 and overexpression is observed in
CC several types of cancer cells and neutrophils/macrophages infiltrating
CC cancerous lesions. Detection of CAAF1 (using antibodies in usual
CC immunoassays) can be used to diagnose (or monitor) inflammation,
CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,
CC lung and cervix), and skin and blood diseases

XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x AAW03564 (1-92)

QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
DB 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
QY 121 CTTCGCAACACCATCAAGAATATCAAAGATAAAGCTGTCTATTGATGAATATTTCCAAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTGACCTTCAAGAAATTCATATCCCTGGTAGCCATT 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGTGAAGGCTGCCCATACCACACCCACAAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 2

AAW24137

ID AAW24137 standard; protein; 92 AA.

XX
AC AAW24137;

XX 28-JAN-1998 (first entry)

XX Human chemotactic cytokine I.

XX chemotactic cytokine; tumour; autoimmune disease; antagonist; agonist.

XX Homo sapiens.

XX WO9723640-A1.

XX 03-JUL-1997.

XX 26-DEC-1995; 95WO-US016871.

XX 26-DEC-1995; 95WO-US016871.

PA (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Alfonso P, Gentz R, Su JY;

XX WPI; 1997-351075/32.

XX N-PSDB; AAT85774.

XX DNA encoding chemotactic cytokine I - used to treat, e.g. tumours,
PT chronic infection, leukaemia, etc.

XX Claim 12; Page 48-49; 64pp; English.

XX This is a human chemotactic cytokine I polypeptide. The encoding
CC polynucleotide, along with a vector and a host cell can be used for the
CC recombinant production of the chemotactic cytokine. Cytokine agonists and
CC antagonists can be used for the treatment of a patient requiring a
CC chemotactic cytokine I and for the treatment of a patient requiring the
CC inhibition of a chemotactic cytokine I polypeptide, respectively. The
CC chemotactic cytokine is used to treat tumours, chronic infection,
CC leukaemia and T-cell mediated autoimmune diseases

XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x AAW24137 (1-92)

QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
DB 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
QY 121 CTTCGCAACACCATCAAGAATATCAAAGATAAAGCTGTCTATTGATGAATATTTCCAAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTGACCTTCAAGAAATTCATATCCCTGGTAGCCATT 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGTGAAGGCTGCCCATACCACACCCACAAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3

AAW45542

ID AAW45542 standard; protein; 92 AA.

XX
AC AAW45542;

XX 22-FEB-2001 (first entry)

XX Human S100A12 protein.

XX S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
KW calcium-binding protein; calcium homeostasis; cardiac muscle;
KW pumping capacity; myocardial cell; systolic calcium ion release;
KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
KW valve defect.

XX Homo sapiens.

XX DE19915485-A1.

XX

PD 19-OCT-2000;
XX
PF 07-APR-1999; 99DE-01015485.
XX
PR 07-APR-1999; 99DE-01015485.
XX
PA (KATU/) KATUS H A.
PA (REMP/) REMPPIS A.
XX
PI Katus HA, Remppis A;
XX
XX
DR WPI; 2000-673510/66.
DR N-PSDB; AAC81812.
XX
PT Composition containing S100 protein, corresponding nucleic acid or
PT vector, useful for treating cardiomyopathy and cardiac insufficiency.
XX
XX
PS Claim 35; Page 20; 36pp; German.
XX
CC This invention describes a novel composition for treating primary or
CC secondary cardiomyopathy or cardiac insufficiency contains at least one
CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
CC fragments, or a gene transfer vector containing (II), optionally
CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
CC proteins involved in calcium homeostasis, so their overexpression in
CC cardiac muscle will improve pumping capacity (and overall capacity) of
CC the heart. In cultured myocardial cells they increase the contraction and
CC relaxation rates associated with increased systolic calcium ion release
CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
CC used to treat cardiomyopathy (CMP) where inherited or caused by
CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
CC by pulmonary and/or arterial hypertension, and structural disease caused
CC by rhythm disorders or valve defects, generally any condition associated
CC with reduced contractile force. Unlike calmodulin, which is expressed
CC ubiquitously, (I) show tissue-specific expression and treat the
CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
CC disease
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-12 (1-276) x AAB45542 (1-92)

QY 1 ATGACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCGCAACACCATCAAGAATATCAAGATATAAGCTGTTCATTGATGAATATTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTCAAGATTTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGCTGCCCATTTACCAACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 4
AAB31911

ID AAB31911 standard; protein; 92 AA.
XX
AC AAB31911;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a human protein.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
XX
OS Homo sapiens.
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-FR002057.
XX
PR 15-JUL-1999; 99FR-00009372.
XX
PA (INMR) BIOMERIEUX STELHYS.
XX
PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX WPI; 2001-159475/16.
DR
XX Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand.
XX
PS Claim 1; Page 168; 209pp; French.
XX
CC The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31911 (1-92)

QY 1 ATGACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCGCAACACCATCAAGAATATCAAGATATAAGCTGTTCATTGATGAATATTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTCAAGATTTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGCTGCCCATTTACCAACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 4
AAB31911

Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTCAAGAAATTCATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 5
AAB31907
ID AAB31907 standard; protein; 92 AA.
XX
AC AAB31907;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a human protein.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthrititis; lupus erythematosus; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-FR002057.
XX
PR 15-JUL-1999; 99FR-00009372.
XX
PA (INMR) BIOMERIEUX STELHYS.
XX
PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX WPI; 2001-159475/16.
XX
DR Detecting, preventing and treating degenerative, neurological and
XX autoimmune diseases, particularly multiple sclerosis, using specified
XX polypeptides or related nucleic acid or ligand.
PS Claim 1; Page 166-167; 209pp; French.
XX
CC The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthrititis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0

DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x AAB31907 (1-92)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGSGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCGCAACACCATCAAGATATCAAGATAAAGCTGTCTCATTGATGAATATTCGAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 6
AAB31908
ID AAB31908 standard; protein; 92 AA.
XX
AC AAB31908;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a human protein.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthrititis; lupus erythematosus; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-FR002057.
XX
PR 15-JUL-1999; 99FR-00009372.
XX
PA (INMR) BIOMERIEUX STELHYS.
XX
PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX WPI; 2001-159475/16.
XX
DR Detecting, preventing and treating degenerative, neurological and
XX autoimmune diseases, particularly multiple sclerosis, using specified
XX polypeptides or related nucleic acid or ligand.
PS Claim 1; Page 167; 209pp; French.
XX
CC The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid

CC polyarthriti and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31908 (1-92)

Qy 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
Qy 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
Qy 121 CTGCAAAACACCATCAAGAATATCAAGATATAAGCTGTCTATTGATGAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
Qy 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAATTTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

Qy 241 GCGCTGAAGGCTGCCCATACCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 7
ADA93649
ID ADA93649 standard; protein; 92 AA.
XX
AC ADA93649;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human calgranulin C protein SEQ ID NO:2.
XX
KW inflammatory disease; calgranulin C; antiinflammatory; gene therapy;
KW vasculitis; Kawasaki disease; cystic fibrosis;
KW chronic inflammatory disease; ulcerative colitis; Crohn's disease;
KW chronic bronchitis; inflammatory arthritis; psoriatic arthritis;
KW rheumatoid arthritis; seronegative arthritis;
KW systemic onset juvenile rheumatoid arthritis; SOJRA; Still's disease;
KW acute inflammation; human.

XX
OS Homo sapiens.
XX
PN WO2003069341-A2.
XX
PD 21-AUG-2003.
XX
PF 17-FEB-2003; 2003WO-EP001575.
XX
PR 15-FEB-2002; 2002US-00077600.
XX
PA (SWIT-) SWITCH BIOTECH AG.
PA (SORG/) SORG C.
PA (ROTH/) ROTH J.
XX
PI Sorg C, Roth J;
XX
DR WPI; 2003-671681/63.
DR N-PSDB; ADA93648.

XX
PT Diagnosing, treating or preventing inflammatory diseases comprises
PT determining the amount and/or concentration of CALGRANULIN C polypeptide
PT and/or nucleic acids encoding the polypeptide present in a biological
PT sample.
XX
PS Claim 7; Page 64; 64pp; English.

XX
CC The present invention describes a method for diagnosing inflammatory
CC diseases, which comprises determining the amount and/or concentration of
CC calgranulin C polypeptide and/or nucleic acids encoding the polypeptide
CC present in the biological sample. Also described are methods for treating
CC or preventing an inflammatory disease in a mammal, and medical treatment
CC of the mammal, where the treatment is based on the stage of the disease
CC to be treated or prevented. Calgranulin C has antiinflammatory activity
CC and can be used in gene therapy. The method is useful for diagnosing,
CC treating or preventing inflammatory diseases, e.g. vasculitis
CC (particularly Kawasaki disease), cystic fibrosis, chronic inflammatory
CC diseases like ulcerative colitis or Crohn's disease, chronic bronchitis,
CC inflammatory arthritis (e.g. psoriatic arthritis, rheumatoid arthritis or
CC seronegative arthritis), systemic onset juvenile rheumatoid arthritis
CC (SOJRA or Still's disease), acute inflammation above the background of a
CC chronic inflammation, an acquired infection on the background of an
CC inflammatory disease, or an exacerbation of an already present disease.
CC The method is also useful for diagnosing specific stages of inflammatory
CC diseases, for determining the risk of relapse, and for discriminating
CC between diseases with similar symptoms. The present sequence represents
CC human calgranulin C, which is used in the exemplification of the present
CC invention.

SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 7 Gaps: 0

US-09-910-208B-12 (1-276) x ADA93649 (1-92)

Qy 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
Qy 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
Qy 121 CTGCAAAACACCATCAAGAATATCAAGATATAAGCTGTCTATTGATGAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
Qy 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAATTTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
Qy 241 GCGCTGAAGGCTGCCCATACCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 8
ADN04192
ID ADN04192 standard; protein; 92 AA.
XX
AC ADN04192;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic protein sequence #291.
XX
KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX OS Homo sapiens.
XX PN WO2004028479-A2.
XX PD 08-APR-2004.
XX PF 25-SEP-2003; 2003WO-US030907.
XX PR 25-SEP-2002; 2002US-0414006P.
XX PA (GETH) GENENTECH INC.
XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX PI Wu TD;
XX WPI; 2004-305105/28.
XX N-PSDB; ADN04191.
XX PT New PRO nucleic acid or polypeptide, useful for preparing a
XX PT pharmaceutical composition for diagnosing or treating psoriasis in a
XX PT mammal.
XX PS Claim 9; SEQ ID NO 586; 3069pp; English.
XX CC The invention relates to novel polynucleotide and polypeptides for
XX CC treating psoriasis or a sequence having at least 80% identity to the
XX CC above sequences. The nucleic acid is useful for preparing a composition
XX CC for diagnosing or treating psoriasis in a mammal. This sequence
XX CC corresponds to one of the polypeptides of the invention.
XX SQ Sequence 92 AA;
Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 8 Gaps: 0
US-09-910-208B-12 (1-276) x ADN04192 (1-92)
QY 1 ATGACAAAACCTTGAGAGCATCTGGAGGGAATTGTCAATATCTTCACCAATACTCAGTT 60
DB 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTGTCAAACACCATCAAGAATATCAAAGATAAAGCTGTCAATGATGAAATATTTCCAAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATT 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTAACACACCCACAAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 9
AD019540
ID AD019540 standard; protein; 92 AA.
XX AC AD019540;
XX AC AD019540;
DT 12-AUG-2004 (first entry)
XX DE Human PRO polypeptide #235.
XX

KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX Homo sapiens.
OS WO2004043361-A2.
XX 27-MAY-2004.
XX PD 06-NOV-2003; 2003WO-US035268.
XX PF 08-NOV-2002; 2002US-0425235P.
XX PR (GETH) GENENTECH INC.
XX PA Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
XX PI Wood WI, Wu TD;
XX WPI; 2004-420067/39.
XX N-PSDB; ADO19539.
XX PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
XX PT treating an immune related disorder such as systemic lupus erythematosus,
XX PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
XX PT spondyloarthropathy.
XX PS Claim 7; SEQ ID NO 470; 1731pp; English.
XX CC The invention relates to human PRO polypeptides and the polynucleotides
XX CC encoding them. The polypeptides and polynucleotides are useful for
XX CC treating and diagnosing immune related disorders in mammals. The immune
XX CC related disorders include systemic lupus erythematosus, rheumatoid
XX CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
XX CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
XX CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
XX CC mellitus, immune-mediated renal disease, demyelinating diseases of the
XX CC central or peripheral nervous system, demyelinating polyneuropathy,
XX CC Guillain-Barre syndrome and chronic inflammatory demyelinating
XX CC polyneuropathy. This sequence represents a human PRO polypeptide of the
XX CC invention.
XX SQ Sequence 92 AA;
Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 8 Gaps: 0
US-09-910-208B-12 (1-276) x ADO19540 (1-92)
QY 1 ATGACAAAACCTTGAGAGCATCTGGAGGGAATTGTCAATATCTTCACCAATACTCAGTT 60
DB 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTGTCAAACACCATCAAGAATATCAAAGATAAAGCTGTCAATGATGAAATATTTCCAAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATT 240

Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGGCTGCCATTACCAACCCACAAAGAG 276
|||||

Db 81 AlaleuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10

ADRI4333

ID ADRI4333 standard; protein; 92 AA.

XX

AC ADRI4333;

XX

DT 21-OCT-2004 (first entry)

XX

DE Human NF-kappaB pathway-associated protein SeqID334.

XX

KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KX antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnery; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; human.

XX

OS Homo sapiens.

XX

PN WO2004065577-A2.

XX

PD 05-AUG-2004.

XX

PF 13-JAN-2004; 2004WO-US000798.

XX

PR 14-JAN-2003; 2003US-0440068P.

PR 12-MAY-2003; 2003US-0469757P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Nadler SG, Neubauer MG, Feder JN, Carman J;

DR WPI; 2004-562168/54.

DR N-PSDB; ADRI4332.

XX

PT New isolated polynucleotides and polypeptides associated with NF-kappaB
pathway, useful for diagnosing, treating, or preventing disorders or
PT diseases associated with NF-kappaB pathway.

XX

PS Claim 6; SEQ ID NO 334; 237pp; English.

XX

CC This invention relates to the novel association of protein sequences (and
CC the genes which encode them) to the NF-kappaB pathway. The invention may
CC be useful for the production of compounds with an antiinflammatory,
CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
CC vulnery activity or for gene therapy. The proteins and nucleotides are
CC useful for diagnosing, preventing, treating, or ameliorating conditions
CC or diseases associated with the NF-kappaB pathway. The condition is an
CC immune disorder, an inflammatory disorder, an inflammatory disorder
CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell

CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
CC immune activity, disorders related to aberrant acute phase responses,
CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
CC organ transplant rejection, conditions related to organ transplant
CC rejection, disorders related to aberrant signal transduction,
CC proliferating disorders, cancers and HIV propagation in cells infected
CC with other viruses. The present sequence is that of a human protein which
CC is subject to the novel association with the NF-kappaB pathway of the
CC invention. Note: This sequence does not appear in the specification but
CC was obtained by the indexer from Genbank.

XX

SQ Sequence 92 AA;

Alignment Scores:

Pred. No.: 4.06e-49 Length: 92

Score: 468.00 Matches: 92

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 98.11% Indels: 0

DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADRI4333 (1-92)

QY 1 ATGACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
|||||

Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGTGCTTACAAAGGC 120
|||||

Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTGCAAAACACCATCAAGAATATCAAAGATAAAGCTGTCTATTGATGAATAATATTCCAAGGC 180
|||||

Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTTCAAGAATTTCATATCCCTGGTAGCCATT 240
|||||

Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGGCTGCCATTACCAACCCACAAAGAG 276
|||||

Db 81 AlaleuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 11

ADP23921

ID ADP23921 standard; protein; 92 AA.

XX

AC ADP23921;

XX

DT 18-NOV-2004 (first entry)

XX

DE PRO polypeptide SEQ ID NO:1099.

XX

KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX

OS Unidentified.

XX

PN WO2004041170-A2.

XX

PD 21-MAY-2004.

XX

PF 30-OCT-2003; 2003WO-US034312.

XX

PR 01-NOV-2002; 2002US-0423394P.

XX

PA (GETH) GENENTECH INC.

XX

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;

XX WPI; 2004-419628/39.
DR N-PSDB; ADP23920.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 7; SEQ ID NO 1099; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteoarthritic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADP23921 (1-92)

QY 1 ATGACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTCCACCAATCTCAGTT 60
Db MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGCATTGTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAACACCATCAAGAATATCAAGATATAAGCTGTCATTGATGAATATTCACAGGC 180
Db LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGCTTCAAGAATTCATATCCCTGGTAGCCATT 240
Db LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGTGCCCATTTACACACCCACAAAGAG 276
Db AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 12
ADS74331

ID ADS74331 standard; protein; 92 AA.
XX
AC ADS74331;
XX
DT 16-DEC-2004 (first entry)
DE PRO polypeptide PRO62943, role in immune-related disease.
XX
KW PRO62943; rheumatoid arthritis; psoriasis; antirheumatic; antiarthritic;
XX antipsoriatic; gene therapy.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 4..47
FT /note= "S-100/ICaBP type calcium binding domain"
FT Region 60..65
FT /note= "N-myristoylation site"
XX
PN WO2004081199-A2.
XX
PD 23-SEP-2004.
XX
PF 10-MAR-2004; 2004WO-US007862.
XX
PR 11-MAR-2003; 2003US-0454025P.
XX
PA (GETH) GENENTECH INC.
XX
XX Baldwin D, Bodary S, Clark H, Fong S, Gurney AL, Williams PM;
PI WPI; 2004-668955/65.
XX N-PSDB; ADS74330.
DR
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating psoriasis, Crohn's disease, Ulcerative Colitis, or rheumatoid
PT arthritis.
XX
PS Claim 9; SEQ ID NO 50; 166pp; English.

XX The present sequence is the protein sequence of novel human PRO
CC polypeptide PRO62943. The invention provides newly identified and
CC isolated nucleotide sequences encoding polypeptides referred to as PRO
CC polypeptides that are useful in the diagnosis and treatment of immune-
CC related diseases. Microarray analysis showed that expression of PRO62943
CC is up-regulated 4-fold in lesional skin as compared to non-lesional skin
CC from psoriasis patients and up-regulated 2-fold in white blood cells from
CC rheumatoid arthritis patients as compared to those from healthy donors.
CC It is also down-regulated 2-fold upon activation of CD4 T cells with CD28
CC or ICAM, down-regulated 6-fold upon differentiation of monocytes into
CC macrophages after 7 days in differentiation media and up-regulated 4-fold
CC upon activation of monocytes with LPS. PRO62943 can be used in a claimed
CC method of identifying a compound that inhibits expression of the gene
CC encoding it. The candidate compound is especially an antisense nucleic
CC acid. The PRO polypeptide can be obtained by recombinant expression,
CC especially in CHO, Escherichia coli or yeast host cells. The polypeptide,
CC its antagonist or an antibody that binds the polypeptide are used in
CC claimed methods for the alleviation or diagnosis of rheumatoid arthritis
CC and psoriasis.

XX SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADS74331 (1-92)

QY 1 ATGACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTCCACCAATCTCAGTT 60

Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTGCAAAACACCATCAAGATATCAAGATATAAGCTGTCATTGATGAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAGAAATTCATATCCCTGGTAGCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGTGAAGGCTGCCATTACCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 13
AAB31909
ID AAB31909 standard; protein; 91 AA.
XX
AC AAB31909;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a human protein.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-FR002057.
XX
PR 15-JUL-1999; 99FR-00009372.
XX
PA (INMR) BIONERIEUX STELHYS.
XX
PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX
DR WPI; 2001-159475/16.
XX
PT Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand.
XX
PS Claim 1; Page 167; 209pp; French.
XX
CC The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells
XX

SQ Sequence 91 AA;
Alignment Scores:
Pred. No.: 1.7e-48 Length: 91
Score: 463.00 Matches: 91
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.06% Indels: 0
DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x AAB31909 (1-91)
QY 4 ACAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 ThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 LysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAAATATCAAAGATAAAGCTGTCAATTGATGAATATTTCCAAGGCCTG 183
Db 41 AlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTGCGACTTTCAGAAATTCATATCCCTGGTAGCATTGCG 243
Db 61 AspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80
QY 244 CTGAAGGCTGCCATTACCACACCCACAAAGAG 276
Db 81 LeuLysAlaAlaHisTyrHisThrHisLysGlu 91
RESULT 14
ID ABG27582 standard; protein; 95 AA.
XX
AC ABG27582;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27573.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 57941; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC

CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 95 AA;

Alignment Scores:
Pred. No.: 7.07e-46 Length: 95
Score: 442.00 Matches: 89
Percent Similarity: 96.74% Conservative: 0
Best Local Similarity: 96.74% Mismatches: 3
Query Match: 92.66% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x ABG27582 (1-95)

QY 1 ATGCAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 4 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIleSerProGln**SerVal 23
QY 61 CGGAAGGGGCATTTTGACACCCCTCTTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 24 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 43
QY 121 CTTGCAACACCATCAAGATATCAAGATATAAGTGTCTATTGATGAATATTTCCAAGGC 180
Db 44 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 63
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAGAAATTCATATCCCTGGTAGCCATT 240
Db 64 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 83
QY 241 GCGCTGAAGGTGCCCATTTACACACCCCAAGAG 276
Db 84 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 95

RESULT 15

AAW01826

ID AAW01826 standard; protein; 91 AA.

XX AC AAW01826;

XX 16-OCT-1997 (first entry)

XX Component of bioactive metal RNA polypeptide.

XX Bioactive; metal; RNA polypeptide; RNP; modulation; analysis;
KW angiogenesis; vascular state; mammalian tissue; transfer; cell;
KW genetic information; selective; alteration; nucleic acid content;
KW leukocyte; pig; monocytic-CuRNP.

OS Sus scrofa.

XX DE19628895-A1.

PN 23-JAN-1997.

PD 17-JUL-1996;

XX 96DE-01028895.

XX 17-JUL-1995; 95DE-01025992.
PR 18-AUG-1995; 95DE-01030500.

XX (FRAU) FRAUNHOFER GBS FOERDERUNG ANGEWANDTEN.

XX Wissler JH, Logemann E, Kiesewetter S, Heilmeyer IMG;

PI WPI; 1997-088586/09.

XX N-PSDB; AAT62569.

DR Bioactive metal RNA polypeptide - useful for modulating angiogenesis,
XX etc.

PS Claim 1; Page 15; 16pp; German.

XX A novel bioactive metal RNA polypeptide (RNP) has a RNA component
CC including the sequence AAT62568 and a polypeptide component having the
CC sequence AAW01826, which is encoded by AAT62569. The RNP, or anti-RNP
CC immunoglobulins, can be used to modulate and/or analyse angiogenesis and
CC the vascular state of mammalian tissue, transfer genetic information in
CC cells and selectively alter the nucleic acid content of cells. Leukocytes
CC from pig's blood were cultured in medium, and the supernatant treated
CC with NH4 sulphate at 35, 45 and 90% saturation to precipitate protein
CC fractions. The residual supernatant was diluted to 45% NH4 sulphate
CC saturation and concentrated by ultrafiltration using a 0.5 kD membrane.
CC The retentate was purified to give 8 mg of product described as monocytic-
CC CuRNP

XX Sequence 91 AA;

Alignment Scores:
Pred. No.: 3.51e-32 Length: 91
Score: 332.00 Matches: 64
Percent Similarity: 81.32% Conservative: 10
Best Local Similarity: 70.33% Mismatches: 17
Query Match: 69.60% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x AAW01826 (1-91)

QY 4 ACAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGGCATTTTGACACCCCTCTTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAACACCATCAAGAATATCAAGATATAAGCTGTCTATTGATGAATATTTCCAAGGCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValLeuValThrAspVal 80
QY 244 CTGAAGGCTGCCCATTTACCACACCCCAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

Search completed: February 23, 2005, 12:08:59

Job time : 115 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: February 23, 2005, 12:13:09 ; Search time 88.5 Seconds
(without alignments)
2041.097 Million cell updates/sec
Title: US-09-910-208B-12
Perfect score: 477
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1380268 seqs, 327241040 residues
Total number of Hits satisfying chosen parameters: 2760536
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool_p/HADDAD-09-910208B/runat_23022005_101937_15400/app_query.fasta.1
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Alignment Scores: 1.22e-48 Length: 92
Pred. No.: 468.00 Matches: 92
Score:

Result No.	Score	Match	Length	DB	ID	Description
1	468	98.1	92	14	US-10-077-600-2	Sequence 2, Appli
2	468	98.1	92	16	US-10-755-889-334	Sequence 334, App
3	309	64.8	90	9	US-09-826-589-3	Sequence 3, Appli
4	309	64.8	90	9	US-09-826-589-4	Sequence 4, Appli
5	309	64.8	90	9	US-09-872-185B-11	Sequence 11, Appl
6	309	64.8	90	9	US-09-872-185B-12	Sequence 12, Appl
7	309	64.8	90	15	US-10-666-513-3	Sequence 3, Appli
8	309	64.8	90	16	US-10-665-867-3	Sequence 3, Appli
9	309	64.8	90	16	US-10-665-867-4	Sequence 4, Appli
10	234	49.1	46	9	US-09-864-761-41579	Sequence 41579, A
11	214.5	45.0	114	9	US-09-214-272-4	Sequence 4, Appli
12	214.5	45.0	114	14	US-10-134-841-4	Sequence 4, Appli
13	214.5	45.0	114	14	US-10-308-279-32	Sequence 32, Appl
14	214.5	45.0	114	15	US-10-116-275-225	Sequence 225, App
15	214.5	45.0	114	15	US-10-131-410-146	Sequence 146, App
16	214.5	45.0	114	15	US-10-424-599-159736	Sequence 159736,
17	214.5	45.0	114	16	US-10-755-889-330	Sequence 330, App
18	194	40.7	95	9	US-09-919-172-102	Sequence 102, App
19	194	40.7	95	9	US-09-981-353-98	Sequence 98, Appl
20	194	40.7	113	15	US-10-276-774-2377	Sequence 2377, Ap
21	189	39.6	50	9	US-09-826-589-2	Sequence 2, Appli
22	189	39.6	50	9	US-09-872-185B-9	Sequence 9, Appli
23	189	39.6	50	15	US-10-666-513-2	Sequence 2, Appli
24	189	39.6	50	16	US-10-665-867-2	Sequence 2, Appli
25	189	39.6	92	10	US-09-492-026-5	Sequence 5, Appli
26	189	39.6	92	10	US-09-919-039-184	Sequence 184, App
27	188	39.4	92	15	US-10-336-603A-102	Sequence 102, App
28	187	39.2	97	16	US-10-363-829-412	Sequence 412, App
29	180.5	37.8	112	14	US-10-205-219-161	Sequence 161, App
30	180.5	37.8	113	10	US-09-492-026-7	Sequence 7, Appli
31	179	37.5	91	14	US-10-106-698-6907	Sequence 6907, Ap
32	178.5	37.4	113	14	US-10-134-841-3	Sequence 3, Appli
33	169.5	35.5	101	9	US-09-393-433-2	Sequence 2, Appli
34	169.5	35.5	101	9	US-09-781-509-2	Sequence 2, Appli
35	169.5	35.5	101	14	US-10-269-643-2	Sequence 2, Appli
36	169.5	35.5	119	13	US-10-087-192-1155	Sequence 1155, Ap
37	168	35.2	477	15	US-10-161-927-62	Sequence 62, Appl
38	161.5	33.9	94	14	US-10-097-340-270	Sequence 270, App
39	158	33.1	93	9	US-09-214-272-2	Sequence 2, Appli
40	158	33.1	93	14	US-10-134-841-2	Sequence 2, Appli
41	158	33.1	93	15	US-10-424-599-273325	Sequence 273325,
42	158	33.1	93	16	US-10-624-631-31	Sequence 31, Appl
43	158	33.1	93	16	US-10-755-889-328	Sequence 328, App
44	157.5	33.0	93	15	US-10-094-886-58	Sequence 58, Appl
45	157.5	33.0	101	9	US-09-393-433-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-077-600-2
; Sequence 2, Application US/10077600
; Publication No. US20030175713A1
; GENERAL INFORMATION:
; APPLICANT: Switch Biotech AG
; TITLE OF INVENTION: Method for diagnosis of inflammatory diseases using Calgranulin
; FILE REFERENCE: S30274US
; CURRENT APPLICATION NUMBER: US/10/077,600
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-077-600-2

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.11%	Indels:	0
DB:	14	Gaps:	0

US-09-910-208B-12 (1-276) x US-10-077-600-2 (1-92)

QY	1	ATGACAAAAC	CTTGAAGAG	CATCTGGAGG	GAATTGTCAATAT	TCTCCACCAAT	ACTCAGTT	60	
Db	1	MetThr	lysLeu	GluGlu	HisLeu	GluGlyIle	ValAsnIle	PheHisGlnTyrSerVal	20
QY	61	CGGAAGGG	GCATTTTGAC	ACCCCTCTCTAAGG	GTGAGTGAAG	CAGCTGCTTACAAAG	GAG	120	
Db	21	ArgLys	GlyHis	PheAsp	ThrLeu	SerLysGly	GluLeu	LysGlnLeuLeuThrLysGlu	40
QY	121	CTTGCAAA	CACCATCA	AGAATATCAAAG	ATAAAGCTGT	CATTGATGAAATAT	TCCAAGGC	180	
Db	41	LeuAla	asnThrIle	LysAsnIle	LysAspLys	AlaValIle	AspGluIle	PheGlnGly	60
QY	181	CTGGATGCT	TAATCAAGAT	GAACAGCTCGACTTTT	CAAGAAATTCATAT	CCCTGGTAGCCATT	240		
Db	61	LeuAsp	AlaAsnGln	AspGluGln	ValAspPhe	GlnGluPheIle	SerLeu	ValAlaIle	80
QY	241	GC	GCTGAAGG	CTGCCCATTTAC	CACCCCAAAAGAG	276			
Db	81	AlaLeu	LysAlaAla	HisTyrHis	ThrHis	LvsGlu	92		

RESULT 2
US-10-755-889-334
; Sequence 334, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 334
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-334

Alignment Scores:		
Pred. No.:	1.22e-48	92
Score:	468.00	92
Percent Similarity:	100.00%	0
Best Local Similarity:	100.00%	0
Query Match:	98.11%	0
DB:	16	0
	Length:	0
	Matches:	0
	Conservative:	0
	Mismatches:	0
	Indels:	0
	Gaps:	0

US-09-910-208B-12 (1-276) x US-10-755-889-334 (1-92)

QY	1	ATGACAAACTTGAAGAGCATCTGGAGGGGAATTGTCAATATCTTCCACCAATACTCAGTT	60
QY	1	MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal	20
Db	1	MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal	20
QY	61	CGGAAGGGGCAATTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG	120
Db	21	ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu	40
QY	121	CTTGCAACACCATCAAGAATATCAAAGATAAAGCTGTCAATTGATGAAATATTCCAAGGC	180
Db	41	LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly	60
QY	181	CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAAATTCATATCCCTGGTAGCCATT	240

Db	61	LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle	80
QY	241	GGCTGAAGCTGCCCATTTACCACACCCACAAGAG	276
Db	81	AlaLeuIvsAlaAlaHisItyrHisThrHisLysGlu	92

RESULT 3
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL R
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Alignment Scores:		
Pred. No.:	4.78e-29	90
Score:	309.00	59
Percent Similarity:	80.00%	13
Best Local Similarity:	65.56%	18
Query Match:	64.78%	0
DB:	9	0
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-09-910-208B-12 (1-276) x US-09-826-589-3 (1-90)

QY	4	ACAAA	CTTGAAGAGCATCTGGAGGGAATTTGTCAATAATCTTCACCACCAATACTCAGTTCGG	63
Db	1	ThrLysLeuGluAspHisLeuGluGlyIleAAsnIlePheHisGlnTySerValArg	20	
QY	64	AAGGG	CATTTTTGACACCCCTCTCTAAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT	123
Db	21	ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu	40	
QY	124	GCAAC	CACCATCAAGAATATCAAAGATAAAGCTGTGCATTTGATGAAATATTCCAAGGCCCTG	183
Db	41	ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu	60	
QY	184	GATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG	243	
Db	61	AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal	80	
QY	244	CTGAAGGCTGCCCATTTACCAACACCCACAAA	273	
Db	81	LeuLysThrAlaHisIleAspIleHisLys	90	

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RESULT 4
US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL R
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine

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US-09-826-589-4 ;
Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-826-589-4 (1-90)

QY 4 ACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 GCAACACCATCAAGAATATCAAAAGATAAAGCTGTCTATTGATGAAATATTCGAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCTAATCAAGATGAACAGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluPheValValLeuValSerArgVal 80

QY 244 CTGAAGGCTGCCATTACCAACCCCAAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 5
US-09-872-185B-11
; Sequence 11, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-11

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-872-185B-11 (1-90)

QY 4 ACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 GCAACACCATCAAGAATATCAAAAGATAAAGCTGTCTATTGATGAAATATTCGAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCTAATCAAGATGAACAGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluPheValValLeuValSerArgVal 80

QY 244 CTGAAGGCTGCCATTACCAACCCCAAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90
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Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCAACCCCAAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 6
US-09-872-185B-12
; Sequence 12, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-12

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-872-185B-12 (1-90)

QY 4 ACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 GCAACACCATCAAGAATATCAAAAGATAAAGCTGTCTATTGATGAAATATTCGAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCTAATCAAGATGAACAGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluPheValValLeuValSerArgVal 80

QY 244 CTGAAGGCTGCCATTACCAACCCCAAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 7
US-10-666-513-3
; Sequence 3, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAG)
; FILE REFERENCE: 0575/55873
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; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Human
US-10-666-513-3

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 15 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-666-513-3 (1-90)
QY 4 ACAAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAATATCAAGATAAAGCTGTTCATTGATGAATATTTCCAAGSCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 8
US-10-665-867-3
; Sequence 3, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-3

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 15 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-665-867-3 (1-90)
QY 4 ACAAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAATATCAAGATAAAGCTGTTCATTGATGAATATTTCCAAGSCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 9
US-10-665-867-4
; Sequence 4, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-4

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-665-867-4 (1-90)
QY 4 ACAAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAATATCAAGATAAAGCTGTTCATTGATGAATATTTCCAAGSCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 10
US-09-864-761-41579
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QY 4 ACAAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAATATCAAGATAAAGCTGTTCATTGATGAATATTTCCAAGSCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 9
US-10-665-867-4
; Sequence 4, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-4

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-665-867-4 (1-90)
QY 4 ACAAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAATATCAAGATAAAGCTGTTCATTGATGAATATTTCCAAGSCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 10
US-09-864-761-41579
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; Sequence 41579, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41579
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011666.18
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.1
; OTHER INFORMATION: EST_HUMAN HIT: AV715719.1, EVALUE 1.00e-19
; OTHER INFORMATION: SWISSPROT HIT: P80511, EVALUE 1.00e-20
US-09-864-761-41579

Alignment Scores:
Pred. No.: 7.24e-20 Length: 46
Score: 234.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 49.06% Indels: 0

DB: 9 Gaps: 0
US-09-910-208B-12 (1-276) x US-09-864-761-41579 (1-46)
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Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
Qy 61 CGGAAGGGGCATTGTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyLeuLysGlnLeuLeuThrLysGlu 40
Qy 121 CTTGCAAAACACCATCAAG 138
Db 41 LeuAlaAsnThrIleLys 46
RESULT 11
US-09-214-272-4
; Sequence 4, Application US/09214272
; Publication No. US20010007674A1
; GENERAL INFORMATION:
; APPLICANT: Siegenthaler, Georges
; TITLE OF INVENTION: Isolated Arachidonic Acid-Binding Heteromer and its Use in
; TITLE OF INVENTION: Cosmetics and Pharmaceuticals
; FILE REFERENCE: 016800-254
; CURRENT APPLICATION NUMBER: US/09/214,272
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: PCT/FR97/01164
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: FR 96/08219
; PRIOR FILING DATE: 1996-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of MRP-14.
US-09-214-272-4

Alignment Scores:
Pred. No.: 2.23e-17 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 9 Gaps: 1

US-09-910-208B-12 (1-276) x US-09-214-272-4 (1-114)

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Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
Qy 121 CTTGCAAAACACCATC--AAGAAATATCAAGATAAAGCTGTCTATTGATGAATATTCCAA 177
Db 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
Qy 178 GGCCTGGATGCTAATCAAGATGAACAGGTCGACTTTCGAAGAATTTCATATCCCTGGTAGCC 237
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
Qy 238 ATTGCGCTGAAGGTCGCCCATTAACACACCCACAAA 273
Db 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96

RESULT 12
US-10-134-841-4

Search completed: February 23, 2005, 12:30:09
Job time : 89.5 secs

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Qy 238 ATTGGCGCTGAAGGCTGCCCATACCACACCCACAAA 273
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Db 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96

RESULT 15
US-10-131-410-146
; Sequence 146, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; TITLE OF INVENTION: TUMORS
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-146

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Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
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Qy 61 CGGAAGGGGCATTTGACACCCCTCTCTAAGGTGAGCTGAAGCAGCTGTACAAAGGAG 120
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Qy 121 CTTGCAAAACACCATC---AAGAATATCAAAGATAAAGCTGTCAATGATGAAATATTCCAA 177
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Db 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
Qy 178 GGCCTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTATATCCCTGGTAGCC 237
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Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
Qy 238 ATTGGCGCTGAAGGCTGCCCATACCACACCCACAAA 273
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Db 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model
Run on: February 23, 2005, 12:02:13 ; Search time 29.5 Seconds
(without alignments)
1396.823 Million cell updates/sec

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Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	468	98.1	92	3	US-09-270-455-20	Sequence 20, Appl	
3	332	69.6	91	3	US-08-794-000-2	Sequence 2, Appli	
4	332	69.6	91	4	US-09-646-651C-1	Sequence 1, Appli	
5	319	66.9	92	2	US-08-568-310D-19	Sequence 19, Appl	
6	319	66.9	92	3	US-09-270-455-19	Sequence 19, Appl	
7	309	64.8	90	4	US-09-263-312-3	Sequence 3, Appli	
8	309	64.8	90	4	US-09-826-589-3	Sequence 3, Appli	
9	309	64.8	90	4	US-09-826-589-4	Sequence 4, Appli	
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12	214.5	45.0	114	4	US-09-806-382A-4	Sequence 4, Appli	

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14	205	43.0	51	2	US-08-568-310D-2	Sequence 2, Appli
15	205	43.0	51	3	US-09-270-455-2	Sequence 2, Appli
16	194	40.7	95	4	US-09-919-172-102	Sequence 102, App
17	194	40.7	95	4	US-09-976-594-467	Sequence 467, App
18	194	40.7	102	4	US-09-949-016-10557	Sequence 10557, A
19	189	39.6	50	4	US-09-263-312-2	Sequence 2, Appli
20	189	39.6	50	4	US-09-826-589-2	Sequence 2, Appli
21	189	39.6	92	2	US-08-918-727-5	Sequence 5, Appli
22	189	39.6	92	3	US-09-205-680A-5	Sequence 5, Appli
23	189	39.6	92	4	US-09-919-039-184	Sequence 184, App
24	187	39.2	92	2	US-09-051-589-1	Sequence 1, Appli
25	184	38.6	91	1	US-07-987-272A-11	Sequence 11, Appl
26	180.5	37.8	113	2	US-08-918-727-7	Sequence 7, Appli
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28	170	35.6	74	4	US-09-513-999C-5490	Sequence 5490, Ap
29	161.5	33.9	131	4	US-09-949-016-11241	Sequence 11241, A
30	158	33.1	93	1	US-07-987-272A-7	Sequence 7, Appli
31	158	33.1	93	1	US-07-987-272A-16	Sequence 16, Appl
32	158	33.1	93	1	US-08-385-241-1	Sequence 1, Appli
33	158	33.1	93	4	US-09-214-272-2	Sequence 2, Appli
34	158	33.1	93	4	US-09-806-382A-3	Sequence 3, Appli
35	157.5	33.0	101	1	US-08-190-560-2	Sequence 2, Appli
36	157.5	33.0	101	1	US-08-469-277-2	Sequence 2, Appli
37	157.5	33.0	101	2	US-08-468-946-2	Sequence 2, Appli
38	157.5	33.0	101	2	US-08-468-942-2	Sequence 2, Appli
39	157.5	33.0	101	4	US-09-298-625-2	Sequence 2, Appli
40	157	32.9	105	2	US-08-918-727-6	Sequence 6, Appli
41	157	32.9	105	3	US-09-205-680A-6	Sequence 6, Appli
42	154	32.3	88	1	US-07-987-272A-1	Sequence 1, Appli
43	154	32.3	89	1	US-07-987-272A-14	Sequence 14, Appl
44	153.5	32.2	97	1	US-07-662-198B-2	Sequence 2, Appli
45	153.5	32.2	110	4	US-09-949-016-11242	Sequence 11242, A

ALIGNMENTS

RESULT 1
US-08-568-310D-20
; Sequence 20, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 20:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-20
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Pred. No.: 6.6e-54 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
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Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTGCAAAACACCATCAAGATATCAAGATAAAGCTGTCAATTCATGAAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTTACCACCCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 2
US-09-270-455-20
Sequence 20, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 20: FROM 1 TO 92
US-09-270-455-20
Alignment Scores:
Pred. No.: 6.6e-54 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
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QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
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Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTTACCACCCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 3
US-08-794-000-2
Sequence 2, Application US/08794000
Patent No. 6087123
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Metal-Containing Ribonucleotide Polypeptides
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,000
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE96/01337
FILING DATE: 17-JUL-1996
CURRENT APPLICATION DATA:
APPLICATION NUMBER: DE 195 25 992.0

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; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 30 500.0
; FILING DATE: 18-AUG-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-794-000-2

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Alignment Scores:		
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US-09-910-208B-12 (1-276) x US-08-794-000-2 (1-91)

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QY	124	GCAACACCATCAAGAATATCAAAAGATAAGCTGTCAATTGATGATAAATATTCCAAGGCGCTG	183
Db	41	ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu	60
QY	184	GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATTGCG	243
Db	61	AspAlaAsnGlnAspGluGlnValserPheLysGluPheValValLeuValThrAspVal	80
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RESULT 4

US-09-646-651C-1
; Sequence 1, Application US/09646651C
; Patent No. 6770455
; GENERAL INFORMATION:
; APPLICANT: Kieseewetter, Stefan
; APPLICANT: Kuhn, Ekehard
; APPLICANT: Koch-Pelster, Brigitte
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
; FILE REFERENCE: 206579
; CURRENT APPLICATION NUMBER: US/09/646,651C
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/EP98/07722
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: DE 198 11 047.2
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..7
; OTHER INFORMATION: Angiotropin-related protein
US-09-646-651C-1

Alignment Scores:

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Pred. No.: 9.86e-36 Length: 91
Score: 332.00 Matches: 64
Percent Similarity: 81.32% Conservative: 10
Best Local Similarity: 70.33% Mismatches: 17
Query Match: 69.60% Indels: 0
DB: 4 Gaps: 0

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QY 124 GCAACACCATCAAGAATATCAAAAGATAAAGCTGTCAATTGATGAA
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLys
QY 184 GATGCTAATCAAGATGAACAGTCGACTTTCAAGAATTCAATATCC
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheVal
QY 244 CTGAAGGCTGCCATTACCAACACCCACAAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 5
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; Sequence 19, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
; TYPE: amino acid
; STRANDEDNESS:

```


TOPOLOGY: linear
MOLECULE TYPE: cdna
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-19

Alignment Scores:
Pred. No.: 5.4e-34 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.88% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x US-08-568-310D-19 (1-92)

QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGlu 40

QY 121 CTGCAACACCATCAAGAATATCAAGATAAAGCTGTCTATGATGAAATATTCACAGGC 180
Db 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg 80

QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276
Db 81 ValLeuLysThrAlaHisIleAspIleHisLysGlu 92

RESULT 6
US-09-270-455-19
Sequence 19, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: cdna
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92
US-09-270-455-19

Alignment Scores:
Pred. No.: 5.4e-34 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.88% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-270-455-19 (1-92)

QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGlu 40

QY 121 CTGCAACACCATCAAGAATATCAAGATAAAGCTGTCTATGATGAAATATTCACAGGC 180
Db 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg 80

QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276
Db 81 ValLeuLysThrAlaHisIleAspIleHisLysGlu 92

RESULT 7
US-09-263-312-3
Sequence 3, Application US/09263312
Patent No. 6555340
GENERAL INFORMATION:
APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: Extracellular No. 6555340el RAGE Binding Protein (EN-RAGE) and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 0575/55873-A
CURRENT APPLICATION NUMBER: US/09/263,312
CURRENT FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 90
TYPE: PRT
ORGANISM: Human
US-09-263-312-3

Alignment Scores:
Pred. No.: 1.16e-32 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-263-312-3 (1-90)

QY 4 ACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAATATCAAGATAAAGCTGTCAATGATGAATATTTCCAAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCCATTTACCACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90
RESULT 8
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3
Alignment Scores:
Pred. No.: 1.16e-32 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x US-09-826-589-3 (1-90)
QY 4 ACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAATATCAAGATAAAGCTGTCAATGATGAATATTTCCAAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCCATTTACCACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90
RESULT 9
US-09-826-589-4
; Sequence 4, Application US/09826589

; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-4
Alignment Scores:
Pred. No.: 1.16e-32 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x US-09-826-589-4 (1-90)
QY 4 ACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAATATCAAGATAAAGCTGTCAATGATGAATATTTCCAAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCCATTTACCACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90
RESULT 10
US-08-385-241-3
; Sequence 3, Application US/08385241
; Patent No. 5776348
; GENERAL INFORMATION:
; APPLICANT: Selengut Ph.D., Jeremy D.
; APPLICANT: Orme-Johnson Ph.D., William H.
; APPLICANT: Dretler M.D., Stephen P.
; APPLICANT: Asakura M.D., Hirotsuka
; TITLE OF INVENTION: SYSTEM AND METHOD FOR INHIBITING
; TITLE OF INVENTION: FORMATION OF CRYSTALLINE STRUCTURES THAT INCLUDE STRUVITE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate, Hall & Stewart
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,241
FILING DATE:


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QY      121 CTGTGCAAAACACCATC---AAGAATAATCAAAGCTCTTCATTGATGAATAATTCCAA 177
Db      45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY      178 GGCCTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAATTATCATATCCCCTGGTAGCC 237
Db      65 AspLeuaspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY      238 ATTGGCGTGAAGGCTGCCCATTTACCACACCCACAAA 273
Db      85 ArgLeuThrTrpAlaSerHisGluLysMethHisGlu 96

RESULT 13
US-07-987-272A-8
; Sequence 8, Application US/07987272A
; Patent No. 5731166
; GENERAL INFORMATION:
; APPLICANT: Geczy, C., Simpson, R. J. and Lackmann, M
; TITLE OF INVENTION: No. 5731166el Chemotactic Factor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman Darby & Cushman
; STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,272A
; FILING DATE: 05-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 2127
; FILING DATE: 05-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 4463
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brinkman, David W
; REGISTRATION NUMBER: 20,817
; REFERENCE/DOCKET NUMBER: DWB/1925/200259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861 3000
; TELEFAX: 202-822 0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-987-272A-8

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Alignment Scores:		
Pred. No.:	2.46e-19	Length: 109
Score:	209.50	Matches: 42
Percent Similarity:	70.33%	Conservative: 22
Best Local Similarity:	46.15%	Mismatches: 26
Query Match:	43.92%	Indels: 1
DB:	1	Gaps: 1

US-09-910-208B-12 (1-276) x US-07-987-272A-8 (1-109)

QY 4 ACAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63

Db 1 SerGlnLeuGluArfAsnIleGluThrIleIleAsnThrPheHisGlnTyrSerValLys 20

QY	64	AAGGGGCATTTTGACACCCCTCTCTAAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT	120
Db	21	LeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAspLeu	40
QY	124	GCAACACCATC---AAGAATATCAAAAGATAAAGCTGTGTCATTGATGAAATATTTCCAAGGC	180
Db	41	GlnAsnPheLeuLysLysGluAsnLysAsnGluLeuValIleGluHisIleMetGluAsp	60
QY	181	CTGGATGCTAATCAAGATGAACAGGTCGACTTTTCAAGAAATTCATATCCCTGGTAGCCATT	240
Db	61	LeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAlaArg	80
QY	241	GCCTGAAGGCTGCCCATTTACACACCCACAAA	273
Db	81	LeuThrTrpAlaSerHisGluLysMetHisGlu	91
RESULT 14			
US-08-568-310D-2			
; Sequence 2, Application US/08568310D			
; Patent No. 5976832			
; GENERAL INFORMATION:			
; APPLICANT: HITOMI, JIRO			
; APPLICANT: YAMAGUCHI, KEN			
; APPLICANT: YAMAMURA, TOKUJIRO			
; APPLICANT: KIMURA, TATSUJI			
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS			
; NUMBER OF SEQUENCES: 20			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE			
; STREET: 99 PARK AVENUE			
; STREET: 6th FLOOR			
; CITY: NEW YORK CITY			
; STATE: NEW YORK			
; COUNTRY: USA			
; ZIP: 10016			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb			
; MEDIUM TYPE: STORAGE			
; COMPUTER: IBM-PC COMPATIBLE			
; OPERATING SYSTEM: PC-DOS 6.2			
; SOFTWARE: WORDPERFECT 6.1			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/568,310D			
; FILING DATE: DECEMBER 6, 1995			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)			
; FILING DATE: 3/6/95 and 3/6/95, respectively			
; ATTORNEY/AGENT INFORMATION:			
; NAME: KLEIN, MILTON			
; REGISTRATION NUMBER: 27101			
; REFERENCE/DOCKET NUMBER: 3316			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (212)953-3350			
; TELEFAX: (212)953-3352			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 51			
; TYPE: amino acid			
; STRANDEDNESS:			
; TOPOLOGY: linear			
; PUBLIC INFORMATION:			
; RELEVANT RESIDUES IN SEQ ID NO: 2:			
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 51			
US-08-568-310D-2			
Alignment Scores:			
Pred. No.:	7.68e-19	Length:	51
Score:	205.00	Matches:	38
Percent Similarity:	90.00%	Conservative:	7
Best Local Similarity:	76.00%	Mismatches:	5
Query Match:	42.98%	Indels:	0

Alignment Scores:	
Pred. No.:	7.68e-19
Score:	205.00
Percent Similarity:	90.00%
Best Local Similarity:	76.00%
Query Match:	42.98%
Length:	51
Matches:	38
Conservative:	7
Mismatches:	5
Indels:	0

US-09-910-208B-12 (1-276) x US-09-270-455-2 (1-51)

Qy 4 ACAAACCTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleAsnIlePheHisGlnTyrSerValArg 20

Qy 64 AAGGGGCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

Qy 124 GCAAACACCATCAAGAATATCAAAAGATAAA 153
Db 41 ProLysThrLeuGlnAsnThrLysAspGln 50

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Job time : 30.5 secs

DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x US-08-568-310D-2 (1-51)

Qy 4 ACAAACCTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleAsnIlePheHisGlnTyrSerValArg 20

Qy 64 AAGGGGCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

Qy 124 GCAAACACCATCAAGAATATCAAAAGATAAA 153
Db 41 ProLysThrLeuGlnAsnThrLysAspGln 50

RESULT 15

US-09-270-455-2

; Sequence 2, Application US/09270455

; Patent No. 6313267

; GENERAL INFORMATION:

; APPLICANT: HITOMI, JIRO

; APPLICANT: YAMAGUCHI, KEN

; APPLICANT: YAMAMURA, TOKUJIRO

; APPLICANT: KIMURA, TATSUJI

; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE

; STREET: 99 PARK AVENUE

; STREET: 6th FLOOR

; CITY: NEW YORK CITY

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb

; MEDIUM TYPE: STORAGE

; COMPUTER: IBM-PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS 6.2

; SOFTWARE: WORDPERFECT 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/270,455

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/568,310

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: KLEIN, MILTON

; REGISTRATION NUMBER: 27101

; REFERENCE/DOCKET NUMBER: 3316

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)953-3350

; TELEFAX: (212)953-3352

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 51

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; PUBLICATION INFORMATION:

; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51

US-09-270-455-2

Alignment Scores:

Pred. No.:	7.68e-19	Length:	51
Score:	205.00	Matches:	38
Percent Similarity:	90.00%	Conservative:	7
Best Local Similarity:	76.00%	Mismatches:	5
Query Match:	42.98%	Indels:	0
DB:	3	Gaps:	0

GenCore version 5.1.6
: Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:26:35 ; Search time 27 Seconds
(without alignments)
1967.098 Million cell updates/sec

Title: US-09-910-208B-12
Perfect score: 92
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Word size: 1
Total number of hits satisfying chosen parameters: 565918

Minimum DB seq length: 0
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-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208B @CGN_1_1_63 @runat_23022005_102316_15808 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	92	JC4712	S-100 calcium-bind
2	9	9.8	91	A55406	calgranulin c - pi
3	9	9.8	122	A42628	calgranulin B - bo
c 4	8	8.8	254	S25281	glTF protein precu
5	8	8.7	404	D82150	conserved hypothet
c 6	8	8.8	525	G95374	probable ABC trans
c 7	8	8.8	900	T39800	probable DNA-bindi
8	8	8.7	962	S03818	carboxymethylcellu
c 9	7	7.7	34	F71350	hypothetical prote
10	7	7.6	50	B34912	hypothetical prote
c 11	7	7.7	111	S69743	probable membrane
12	7	7.6	132	A48418	interleukin-5 prec
13	7	7.6	133	ICMS5	interleukin-5 prec
c 14	7	7.7	147	S72253	hemoglobin, extrac

15	7	7.6	159	2	A64476	hypothetical prote
16	7	7.6	165	2	H90418	hypothetical prote
c 17	7	7.7	173	2	E90625	NADH dehydrogenase
18	7	7.6	174	2	T41632	probable calcineur
19	7	7.6	175	2	JH0462	phosphoprotein pho
c 20	7	7.7	177	2	H75568	phosphoribosylamin
c 21	7	7.7	183	2	SS2904	virion protein j13
c 22	7	7.7	197	2	S61614	probable membrane
c 23	7	7.7	225	1	BVECAM	membrane protein a
c 24	7	7.7	225	2	H90683	arOM protein limpo
c 25	7	7.7	225	2	D85534	protein of aro ope
26	7	7.6	276	2	H71985	pantoate-beta-alan
27	7	7.6	276	2	G64533	hypothetical prote
c 28	7	7.7	282	2	A85076	hypothetical prote
29	7	7.6	288	2	T48753	conserved hypothet
c 30	7	7.7	293	2	T48975	xyloglucan endo-tr
31	7	7.6	299	2	AD1833	methylenetetrahydr
32	7	7.6	310	2	A70449	hypothetical prote
c 33	7	7.7	315	2	D64018	hypothetical prote
34	7	7.6	318	2	B82447	conserved hypothet
c 35	7	7.7	319	2	A84204	phosphate ABC tran
36	7	7.6	334	2	A83225	binding protein co
37	7	7.6	335	2	S48061	DNA-directed DNA p
38	7	7.6	339	2	T17113	NADH2 dehydrogenas
39	7	7.6	350	2	T29436	hypothetical prote
40	7	7.6	353	2	B89973	hypothetical prote
c 41	7	7.7	355	2	A97506	hypothetical prote
c 42	7	7.7	355	2	AE2724	hypothetical prote
c 43	7	7.7	358	2	G75586	urea/short chain-a
44	7	7.6	366	2	AE3211	hypothetical prote
45	7	7.6	367	2	T36116	probable oxidoredu
46	7	7.6	373	2	F64594	8-amino-7-oxononan
c 47	7	7.7	373	2	T16529	hypothetical prote
c 48	7	7.7	383	2	A95211	transcription regu
c 49	7	7.7	383	2	C98075	conserved hypothet
c 50	7	7.7	401	2	T46306	hypothetical prote
51	7	7.6	409	2	AG0362	manganese transpor
52	7	7.6	442	2	T22632	hypothetical prote
c 53	7	7.7	443	2	AF2884	hypothetical prote
c 54	7	7.7	443	2	C97660	hypothetical prote
55	7	7.6	447	2	A47430	gastrin/cholecysto
56	7	7.6	452	2	JC2459	gastrin/cholecysto
57	7	7.6	453	2	S32817	gastrin receptor -
c 58	7	7.7	458	2	B81325	probable C4-dicarb
c 59	7	7.7	458	2	T02804	hypothetical prote
60	7	7.6	465	2	T48374	UDPG glucosyltrans
61	7	7.6	470	2	T07605	protein farnesyltr
62	7	7.6	470	2	T07673	farnesyltranstrans
63	7	7.6	478	2	H71261	conserved hypothet
64	7	7.6	482	1	VGXPT7	surface glycoprote
65	7	7.6	483	1	VGXPT5	surface glycoprote
66	7	7.6	483	1	VGXPTV	surface glycoprote
67	7	7.6	483	2	AD1223	hypothetical prote
c 68	7	7.7	509	2	T05260	probable disease r
69	7	7.6	523	2	B55194	importin 2 - Afric
c 70	7	7.7	523	2	S64826	probable membrane
c 71	7	7.7	542	2	T35938	probable substrate
c 72	7	7.7	549	1	H65214	probable Na+/H+ ex
c 73	7	7.7	549	2	C86100	hypothetical prote
c 74	7	7.7	549	2	G91259	hypothetical prote
c 75	7	7.7	550	2	B90174	DNA helicase limpo
76	7	7.6	601	2	S77459	ABC-type transport
c 77	7	7.7	678	1	B75360	2',3'-cyclic-nucle
c 78	7	7.7	822	2	B97839	ATP-dependent heli
c 79	7	7.7	842	2	T41697	translation elonga
c 80	7	7.7	869	2	A71400	probable disease r
81	7	7.6	1051	2	T13174	gp150 protein - fr
82	7	7.6	1083	2	T00790	ubiquitin-specific
83	7	7.6	1123	1	SYNCLC	leucine-tRNA ligas
84	7	7.6	1130	2	A69836	DNA exonuclease ho
c 85	7	7.7	1157	2	T40572	protein phosphatas
86	7	7.6	1188	2	G83960	chromosome segrega
c 87	7	7.7	1266	2	I59314	isoleucine-tRNA li

88	7	1335	7.6	2	T18289	racGAP protein - s	161	6	6.5	129	2	I37779	Ig variable region
89	7	1450	7.6	2	T45888	ABC transporter-li	162	6	6.5	129	2	S75257	hypothetical prote
90	7	1504	7.6	2	T17426	FK506 polyketide s	163	6	6.5	132	2	T44301	hypothetical prote
91	7	1647	7.6	2	T41267	hypothetical prote	c 164	6	6.6	133	2	A89981	hypothetical prote
92	7	1674	7.7	2	G96736	hypothetical prote	165	6	6.5	135	2	H97156	transcription term
93	7	2254	7.6	2	D86215	protein T6D22.14 l	166	6	6.5	135	2	I64147	lactoylglutathione
94	6	35	6.6	2	E70243	hypothetical prote	c 167	6	6.6	136	2	E83766	hypothetical prote
95	6	40	6.5	2	I39944	regulatory extrace	c 168	6	6.6	137	2	G75471	hypothetical prote
96	6	45	6.6	2	E90956	hypothetical prote	c 169	6	6.6	138	2	S09258	Ig heavy chain V r
97	6	45	6.6	2	D82788	hypothetical prote	c 170	6	6.6	138	2	S17941	export protein xps
98	6	46	6.5	2	A26929	sacQ protein - Bac	c 171	6	6.6	138	2	AD0281	conserved hypothet
99	6	47	6.6	2	A22162	complement C3 - ra	172	6	6.5	139	2	S69458	hypothetical prote
100	6	53	6.5	2	PH0107	straight pilin - A	c 173	6	6.6	140	2	T01170	ferredoxin [2Fe-2S
101	6	58	6.6	2	S78711	protein YDR034c-a	174	6	6.5	141	2	E55855	lysA protein - pha
102	6	59	6.6	2	C72663	hypothetical prote	175	6	6.5	141	2	E75336	aminoglycoside ace
103	6	61	6.6	2	AC2666	hypothetical prote	c 176	6	6.6	141	2	F83675	hypothetical prote
104	6	65	6.5	2	AC0576	conserved hypothet	c 177	6	6.6	142	2	T27038	hypothetical prote
105	6	69	6.5	2	H81436	phnA-like protein	178	6	6.5	142	2	H71022	hypothetical prote
106	6	72	6.5	2	AE2771	hypothetical prote	c 179	6	6.6	143	2	S03747	small membrane pro
107	6	73	6.6	1	WSWL18	E5 protein - human	180	6	6.5	145	1	B64330	hypothetical prote
108	6	75	6.5	2	E90974	probable cell divi	c 181	6	6.6	145	2	T22373	hypothetical prote
109	6	78	6.5	1	A40850	secretory protein	182	6	6.5	145	2	T50276	hypothetical prote
110	6	79	6.5	2	G86722	hypothetical prote	183	6	6.5	147	2	T28131	hypothetical prote
111	6	79	6.5	2	S75193	hypothetical prote	184	6	6.5	148	2	AH0712	hypothetical prote
112	6	83	6.6	2	F71485	hypothetical prote	185	6	6.5	148	2	F85789	probable membrane
113	6	85	6.6	2	I40691	immunity protein 8	186	6	6.5	148	2	B90941	hypothetical prote
114	6	87	6.5	2	D61547	hypothetical prote	187	6	6.5	148	2	E64939	hypothetical prote
115	6	87	6.6	2	T17874	hypothetical prote	c 188	6	6.6	149	2	D83758	transcription regu
116	6	90	6.5	2	T17643	hypothetical prote	c 189	6	6.6	149	2	B71067	hypothetical prote
117	6	93	6.5	2	AG1442	protein gp41 (Bact	c 190	6	6.6	150	2	S29890	Ribosomal protein
118	6	95	6.5	1	S35985	S-100 protein alph	191	6	6.5	150	2	JC4243	transcription CCAA
119	6	95	6.6	2	AG0277	probable phage-rel	c 192	6	6.6	152	2	B26471	Ig heavy chain pre
120	6	96	6.6	2	H86681	prophage pil prote	193	6	6.5	152	2	AH3245	conserved hypothet
121	6	97	6.5	2	A30129	S-100 protein, lun	194	6	6.5	153	2	B84043	hypothetical prote
122	6	98	6.5	2	I40616	DNA-binding protei	c 195	6	6.6	154	2	D89406	protein F16H6.10 l
123	6	98	6.5	2	A41988	S-100 calcium-bind	c 196	6	6.6	154	2	T21023	hypothetical prote
124	6	100	6.6	2	A84949	NADH2 dehydrogenas	197	6	6.5	155	2	B70370	hypothetical prote
125	6	100	6.5	2	T48706	hypothetical prote	198	6	6.5	157	2	AC1665	shikimate kinase h
126	6	100	6.6	2	T49857	hypothetical prote	c 199	6	6.6	157	2	H72650	hypothetical prote
127	6	101	6.5	2	G72759	hypothetical prote	c 200	6	6.6	158	2	G87623	chemotaxis protein
128	6	103	6.6	2	T10397	protein gp16 - Org	201	6	6.5	159	2	C81662	cytosolic acyl-CoA
129	6	105	6.6	2	D82962	hypothetical prote	c 202	6	6.6	159	2	A72709	hypothetical prote
130	6	105	6.6	2	A83175	hypothetical prote	c 203	6	6.6	160	1	C63252	conserved hypothet
131	6	105	6.5	2	S40282	protein-tyrosine-p	c 204	6	6.6	160	2	B64225	dihydrofolate redu
132	6	106	6.5	2	T10224	hypothetical prote	205	6	6.5	160	2	E82565	hypothetical prote
133	6	106	6.6	2	S76805	hypothetical prote	206	6	6.6	161	2	A83066	hypothetical prote
134	6	106	6.6	2	B64001	hypothetical prote	c 207	6	6.6	162	1	B41659	benzoate 1,2-dioxy
135	6	106	6.6	2	JV0105	hypothetical prote	c 208	6	6.6	162	2	I39170	cyclin A/CDK2-asso
136	6	108	6.6	2	S75384	hypothetical prote	c 209	6	6.6	163	2	A57630	transcription-asso
137	6	108	6.6	2	F69969	hypothetical prote	c 210	6	6.5	166	2	JN0248	platelet-derived g
138	6	111	6.6	2	F70338	methionine-tRNA li	c 211	6	6.6	166	2	H96739	hypothetical prote
139	6	112	6.5	2	B96951	similar to arsenat	c 212	6	6.6	168	2	T07640	PEARLI 1 protein -
140	6	114	6.5	2	B31848	calgranulin B [val	213	6	6.5	168	2	A34952	CS3 fimbrial prote
141	6	115	6.6	2	T17090	NADH2 dehydrogenas	c 214	6	6.6	168	2	H83075	type 4 fimbrial bi
142	6	115	6.6	2	S04754	NADH2 dehydrogenas	c 215	6	6.6	168	2	C72470	hypothetical prote
143	6	115	6.6	2	D71194	hypothetical prote	216	6	6.5	169	2	I50166	B-G antigen - chic
144	6	117	6.6	1	HVMS39	Ig heavy chain pre	c 217	6	6.6	169	2	T33727	conserved hypothet
145	6	117	6.6	1	HVMS57	Ig heavy chain pre	c 218	6	6.6	170	2	A57277	beta-3 endonexin,
146	6	117	6.6	1	HVMS84	Ig heavy chain pre	c 219	6	6.6	171	2	AC0824	chaperone protein
147	6	117	6.6	1	S66720	probable membrane	220	6	6.5	171	2	JQ1995	envelope protein V
148	6	118	6.6	2	E71158	hypothetical prote	221	6	6.5	171	2	B87018	probable membrane
149	6	118	6.6	2	G02438	D-dopachrome tauto	c 222	6	6.6	171	2	T18167	hypothetical prote
150	6	118	6.5	2	JE0162	dopachrome isomera	223	6	6.5	171	2	T15894	hypothetical prote
151	6	120	6.6	2	A61301	histone H2B - Tetr	224	6	6.5	172	2	A71263	hypothetical prote
152	6	121	6.6	2	F84133	hypothetical prote	225	6	6.5	172	2	AB2848	hypothetical prote
153	6	122	6.5	2	A27097	histone H2B.1 - Te	c 226	6	6.6	172	2	AB3214	ABC transporter, s
154	6	122	6.6	2	B27097	histone H2B.2 - Te	c 227	6	6.6	173	2	T11336	NADH2 dehydrogenas
155	6	122	6.6	2	AB1416	transcription regu	228	6	6.5	174	2	T47245	calcineurin regula
156	6	122	6.6	2	A11791	transcription regu	229	6	6.5	174	2	D84676	hypothetical prote
157	6	122	6.6	2	D71183	hypothetical prote	230	6	6.5	176	2	E72565	hypothetical prote
158	6	124	6.6	2	S49604	hypothetical prote	c 231	6	6.6	176	2	T21573	hypothetical prote
159	6	125	6.6	2	S52255	copper resistance	232	6	6.5	176	2	D71146	hypothetical prote
160	6	126	6.6	2			c 233	6	6.6	177	2	T07642	PEARLI 1 protein h

c 234	6	6.6	177	2	S25845	dimerase - Strepto	307	6	6.5	215	2	S08220	platelet-derived g
235	6	6.5	177	2	S74636	hypothetical prote	c 308	6	6.6	215	2	T36153	probable permease
236	6	6.5	178	2	S44624	C50C3.5 protein -	c 309	6	6.6	215	2	G81993	hypothetical prote
237	6	6.5	179	2	C83425	hypothetical prote	c 310	6	6.6	215	2	G81223	conserved hypothet
c 238	6	6.6	180	2	T50530	hypothetical prote	311	6	6.5	216	2	AG2591	peptide methionine
239	6	6.5	182	2	T36540	probable orotate p	312	6	6.5	218	2	T01076	transcription fact
240	6	6.5	183	2	T51495	hypothetical prote	313	6	6.5	218	2	A36673	immunoglobulin enh
c 241	6	6.6	183	2	JH0803	tyrosine kinase re	c 314	6	6.5	219	2	S27332	proteasome endopep
242	6	6.5	183	2	C75082	hypothetical prote	315	6	6.6	220	2	G85872	probable lipoprote
243	6	6.5	184	2	H83631	conserved hypothet	316	6	6.5	220	2	T08628	hypothetical prote
244	6	6.5	184	2	E90035	hypothetical prote	317	6	6.5	220	2	T26434	hypothetical prote
c 245	6	6.6	185	2	E69884	hypothetical prote	c 318	6	6.6	221	2	B64188	arginine transport
246	6	6.5	185	2	T34286	hypothetical prote	319	6	6.6	221	2	T15848	hypothetical prote
247	6	6.5	186	2	G86154	hypothetical prote	320	6	6.5	221	2	H83608	probable transcrip
248	6	6.5	186	2	B75421	probable pilin, ty	321	6	6.5	223	2	C82555	heme ABC transport
249	6	6.5	187	2	H97478	cycL protein [limpo	c 322	6	6.6	223	2	H95106	conserved hypothet
250	6	6.5	188	2	A70256	hypothetical prote	c 323	6	6.6	223	2	F83703	hypothetical prote
c 251	6	6.6	189	2	A69272	tungsten formylmet	c 324	6	6.6	223	2	B97975	hypothetical prote
c 252	6	6.6	189	2	D75213	hypothetical prote	c 325	6	6.6	224	2	B87197	hypothetical prote
c 253	6	6.6	190	2	H75162	anthranilate synth	c 326	6	6.6	224	2	E70790	probable transcrip
254	6	6.5	190	2	T43172	hypothetical prote	327	6	6.5	224	2	C97587	succinoglycan bios
c 255	6	6.6	192	2	F71169	probable protein-t	c 328	6	6.6	226	1	JQ1570	major surface anti
c 256	6	6.6	193	2	JQ2185	coat protein - app	c 329	6	6.6	226	1	JQ1573	major surface anti
257	6	6.5	193	2	S01975	gene D5 protein -	c 330	6	6.6	226	1	JQ1578	major surface anti
c 258	6	6.6	194	2	S59793	SKP1 protein - yea	c 331	6	6.6	226	1	JQ1579	major surface anti
259	6	6.5	194	2	A64331	hypothetical prote	c 332	6	6.6	226	1	JQ1580	major surface anti
260	6	6.5	195	2	B86469	protein F12K21.10	c 333	6	6.6	226	1	JQ1581	3-dehydroquinat d
261	6	6.5	195	2	A96731	unknown protein F5	334	6	6.5	226	2	B86830	platelet-derived g
262	6	6.5	195	2	AE3074	transcription regu	335	6	6.5	226	2	I51550	surface antigen -
263	6	6.5	196	2	A37359	platelet-derived g	c 336	6	6.6	226	2	JQ2058	surface antigen -
264	6	6.5	196	2	A48851	platelet-derived g	c 337	6	6.6	226	2	JQ2087	surface antigen -
265	6	6.5	196	2	B28964	platelet-derived g	c 338	6	6.6	226	2	JQ2089	surface antigen -
266	6	6.5	196	2	T50018	MADS box protein F	c 339	6	6.6	226	2	JQ2085	surface antigen -
267	6	6.5	197	2	S25096	platelet-derived g	c 340	6	6.6	226	2	JQ2119	surface antigen -
268	6	6.5	197	2	F82921	conserved hypothet	c 341	6	6.6	226	2	JQ2092	surface antigen -
269	6	6.5	197	2	S73688	hypothetical prote	c 342	6	6.6	226	2	JQ2061	surface antigen -
270	6	6.5	197	2	AE2808	succinoglycan bios	c 343	6	6.6	226	2	JQ2116	surface antigen -
c 271	6	6.6	197	2	S48377	probable membrane	c 344	6	6.6	226	2	JQ2225	small surface prot
c 272	6	6.6	197	2	D86316	protein T10022.9 [c 345	6	6.6	226	2	JQ2060	surface antigen -
273	6	6.5	197	2	H83038	hypothetical prote	c 346	6	6.6	226	2	JQ2090	surface antigen -
274	6	6.5	198	2	AH2696	cycL protein [limpo	c 347	6	6.6	226	2	JQ2091	surface antigen -
275	6	6.5	198	2	JS0735	platelet-derived g	c 348	6	6.6	226	2	JQ2121	surface antigen -
276	6	6.5	198	2	I39670	rolD protein - Agr	c 349	6	6.6	226	2	JQ2057	surface antigen -
c 277	6	6.6	199	2	A97310	probable cAMP-bind	c 350	6	6.6	226	2	JQ2088	surface antigen -
278	6	6.5	199	2	D98212	probable tetr-fami	c 351	6	6.6	226	2	JQ2110	surface antigen -
279	6	6.5	200	2	I51551	platelet-derived g	c 352	6	6.6	226	2	JQ2062	surface antigen -
280	6	6.5	202	2	T31452	probable 4-vinyl r	c 353	6	6.6	226	2	JQ2059	surface antigen -
281	6	6.5	202	2	T50396	conserved hypothet	c 354	6	6.6	226	2	G96789	protein T23E18.14
282	6	6.5	202	2	A90139	hypothetical prote	c 355	6	6.5	227	2	G69762	two-component resp
283	6	6.5	204	2	I50163	B-G antigen - Chic	356	6	6.5	227	2	D84943	hypothetical protei
284	6	6.5	207	2	AF0080	probable exported	357	6	6.5	228	2	S60639	cytochrome-c oxida
c 285	6	6.6	207	2	JQ0397	nods protein - Azo	358	6	6.5	228	2	H97373	hypothetical prote
286	6	6.5	207	2	F90093	U3 snRNP protein	359	6	6.5	228	2	S45677	proteinase inhibit
c 287	6	6.6	208	2	D71529	probable anthranil	c 360	6	6.6	229	2	G82420	arginine ABC trans
c 288	6	6.6	209	2	A55632	proteasome LMP2.s	361	6	6.5	229	2	S41086	translation elonga
289	6	6.5	209	2	S04827	gene 40A protein -	c 362	6	6.6	229	2	F64398	hypothetical prote
290	6	6.5	209	2	I50223	enhancer binding p	363	6	6.5	230	2	H97838	DNA-directed DNA p
c 291	6	6.6	211	1	S40836	formate dehydrogen	c 364	6	6.5	231	2	T03752	hypothetical prote
292	6	6.5	211	1	PFHUG1	platelet-derived g	365	6	6.5	231	2	AD0773	hypothetical prote
293	6	6.5	211	1	XMECDD	dedD protein - Esc	c 366	6	6.6	231	2	E86338	protein F5M15.16 [
c 294	6	6.6	211	2	AD0946	formate dehydrogen	367	6	6.5	232	2	S43188	orotidine-5'-phosp
c 295	6	6.6	211	2	B91231	formate dehydrogen	368	6	6.5	232	2	B83285	orotidine 5'-phosp
c 296	6	6.6	211	2	A86078	formate dehydrogen	369	6	6.5	232	2	AH0026	30S ribosomal prot
297	6	6.5	211	2	F91028	probable lipoprote	370	6	6.5	232	2	D72037	macromolecule tran
c 298	6	6.6	211	2	D69397	GTP-binding protei	371	6	6.5	232	2	G86588	macromolecule tran
c 299	6	6.6	212	2	F84481	Mutator-like trans	c 372	6	6.6	232	2	G69703	sapB protein [limpo
c 300	6	6.6	212	2	E83936	hypothetical prote	373	6	6.5	232	2	AE2456	hypothetical prote
301	6	6.5	213	2	S76070	hypothetical prote	374	6	6.5	233	1	R3EC3	ribosomal protein
302	6	6.5	213	2	AB2213	hypothetical prote	375	6	6.5	233	2	G85996	30S ribosomal subu
303	6	6.5	213	2	A83614	hypothetical prote	376	6	6.5	233	2	AG1006	30S ribosomal chai
c 304	6	6.6	213	2	T44588	hypothetical prote	377	6	6.5	233	2	C91151	30S ribosomal subu
c 305	6	6.6	214	2	T51061	hypothetical transcrip	378	6	6.5	234	2	S76625	hypothetical prote
c 306	6	6.6	215	2	A29318	ubiquinol-cytochro	379	6	6.5	235	2	S26300	transcription fact

transcription fact 236 2 T48518
protein Y106G6H.14 236 2 AB07976
phosphoribosylamin 237 2 H71974
hypothetical prote 237 2 A64532
hypothetical prote 237 2 G75316
probable lipase - 237 2 C83880
hypothetical prote 237 2 AD1368
amino acid ABC-tra 238 2 AE1737
amino acid ABC-tra 238 2 A71216
hypothetical prote 239 2 AE1381
lipolytic enzyme h 239 2 AC2745
glycerophosphoryl 240 2 H69846
hypothetical prote 240 2 C64609
ABC transporter, A 240 2 G71905
probable ABC trans 241 1 S06998
acetoacetyl-CoA re 241 2 F91287
hypothetical prote 241 2 A86129
hypothetical prote 241 2 S56536
hypothetical prote 241 2 F96631
lumQ protein - Syn 241 2 S77548
spherulin 1b precu 243 2 B29624
hypothetical prote 243 2 F71876
hypothetical prote 243 2 AE3004
hypothetical prote 243 2 AD1983
hypothetical prote 245 2 D98279
hypothetical prote 246 2 S47805
hypothetical 27.4K 246 2 D91186
probable outer mem 246 2 C86033
probable exported 246 2 AF0542
hypothetical prote 246 2 C90660
probable membrane 246 2 A64747
hypothetical prote 246 2 A85511
hypothetical prote 246 2 T16941
hypothetical prote 246 2 T30660
hypothetical prote 246 2 B97526
hypothetical prote 247 2 F70626
carboxylesterase (247 2 JC1374
granzyme C (EC 3.4 248 1 PRMSC2
spherulin 1a precu 248 2 A29624
granzyme M (EC 3.4 249 2 A55634
transcription regu 251 2 G82481
hypothetical prote 253 2 G75008
conserved hypothet 253 2 B69758
hypothetical prote 253 2 C69288
major prion PrP-Sc 254 1 UJHYIH
glycerol uptake fa 254 2 H70129
hypothetical zinc 254 2 T37951
29.0K hypothetical 254 2 H86458
conserved hypothet 255 2 E82363
conserved hypothet 255 2 AG3109
conserved hypothet 256 2 A71301
BR1 protein - toma 257 1 JQ1873
short chain dehydr 257 2 AD2934
reductase (AL13282 257 2 C98348
major prion prp27- 257 2 A23545
hypothetical prote 257 2 G84712
CT262 hypothetical 259 2 A86542
conserved hypothet 259 2 B72083
gene 2 protein - M 259 2 S30950
hypothetical prote 260 2 C83362
short chain dehydr 261 2 T41116
hypothetical prote 261 2 S69709
SN-glycerol-3-phos 261 2 F69090
cytochrome-c oxida 262 2 T11355
probable carboxype 262 2 A64882
probable carboxype 262 2 H85751
probable carboxype 262 2 A99867
alkylphosphonate A 263 2 G84021
dihydrodipicolinat 264 2 F72002
conserved hypothet 264 2 D86621
conserved hypothet 264 2 H70434
conserved hypothet 265 2 AF2928

453 6 6.5 H98353
c 454 6 6.6 A81531
455 6 6.5 S63621
c 456 6 6.6 S75243
457 6 6.5 B69781
458 6 6.5 JX0316
c 459 6 6.6 S67622
c 460 6 6.6 S20069
461 6 6.6 A82257
462 6 6.5 C97028
463 6 6.5 F64520
c 464 6 6.6 G47301
c 465 6 6.6 C84426
466 6 6.5 A82942
467 6 6.5 AE2012
c 468 6 6.6 Z2BP73
469 6 6.6 E75546
c 470 6 6.6 G75177
471 6 6.5 AB3307
472 6 6.5 AB2254
c 473 6 6.6 C64620
c 474 6 6.6 B71894
c 475 6 6.6 S26203
c 476 6 6.5 AH1677
c 477 6 6.6 S46059
c 478 6 6.6 JQ2226
479 6 6.5 T29825
480 6 6.5 T19933
481 6 6.5 B81288
482 6 6.5 B64694
c 483 6 6.6 S67062
484 6 6.5 JC6206
485 6 6.5 DNA restriction en
486 6 6.5 ethanolamine ammon
c 487 6 6.6 conserved hypothet
488 6 6.5 hypothetical prote
c 489 6 6.6 hypothetical prote
490 6 6.5 NADH2 dehydrogenas
491 6 6.5 hypothetical prote
c 492 6 6.5 conserved hypothet
493 6 6.6 RepA protein - Esc
c 494 6 6.6 methionine aminope
c 495 6 6.6 methionine aminope
c 496 6 6.6 probable methionin
497 6 6.5 hypothetical prote
498 6 6.5 yfjB protein - Esc
499 6 6.5 conserved hypothet
500 6 6.5 conserved hypothet

ALIGNMENTS

RESULT 1

JC4712
S-100 calcium-binding protein Al2 - human
N;Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; calg
utrophil protein
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4712; JC4717; JC4891; S56113; S56114
R;Yamamura, T.; Hitomi, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsukada,
Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A;Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping.
A;Reference number: JC4712; MUID:96192053; PMID:8619860
A;Accession: JC4712
A;Molecule type: mRNA
A;Residues: 1-92 <YAM>
A;Cross-references: UNIPROT:P80511; DDBJ:D83657; NID:g1502284; PIDN:BAAL2030.1; PID:g150
R;Marti, T.; Erttmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A;Title: Host-parasite interaction in human onchocerciasis: Identification and sequence
A;Reference number: JC4717; MUID:96192069; PMID:8619876
A;Accession: JC4717

A;Molecule type: protein
A;Residues: 2-92 <MAR>
A;Experimental source: Onchocerca volvulus infecting human tissue
R;ILg, E.C.; Troxler, H.; Buergliesser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hunzel
Biochem. Biophys. Res. Commun. 225, 146-150, 1996
A;Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP, C
A;Reference number: JC4891; MUID:96332419; PMID:8769108
A;Accession: JC4891
A;Molecule type: protein
A;Residues: 2-92 <ILG>
R;Guignard, F.; Mauel, J.; Markert, M.
Biochem. J. 309, 395-401, 1995
A;Title: Identification and characterization of a novel human neutrophil protein related
A;Reference number: S56113; MUID:95351965; PMID:7626002
A;Accession: S56113
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'XX',4-14,'X',16-17,'XXXX' <GUI1>
A;Experimental source: isoform 6a
A;Accession: S56114
A;Status: preliminary
A;Molecule type: protein
A;Residues: 2-21 <GUI2>
A;Experimental source: isoform 6b
A;Comment: This protein is released by activated neutrophils in the course of inflammato
C;Genetics:
A;Gene: GDB:S100A12; p6; MRP6; CGRP; CAAF1
A;Cross-references: GDB:5218374
A;Map position: 1q21-1q21
C;Complex: monomer
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
F;2-92/Product: 8-100 calcium-binding protein A12 #status experimental <MAT>
F;6-39/Domain: calmodulin repeat homology <EF1>
F;49-81/Domain: calmodulin repeat homology <EF2>
F;86-90/Region: zinc binding #status predicted

Alignment Scores:
Pred. No.: 2.36e-91 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x JC4712 (1-92)

Qy 1 ATGACAAACTTGAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

Qy 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

Qy 121 CTGCAAAACACCATCAAGAATATCAAAGATAAAGCTGTCATTGATGAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

Qy 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

Qy 241 GCGCTGAAGGCTGCCCATACCACACCCACAAGAG 276
Db 81 AlaleuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 2
A55406
calgranulin c - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55406

R;Dell'Angelica, E.C.; Schleicher, C.H.; Santome, J.A.
J. Biol. Chem. 269, 28929-28936, 1994
A;Title: Primary structure and binding properties of calgranulin C, a novel S100-like c
A;Reference number: A55406; MUID:95050708; PMID:7961855
A;Accession: A55406
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-91
A;Cross-references: UNIPROT:P80310
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand
F;48-80/Domain: calmodulin repeat homology <EF2>

Alignment Scores:
Pred. No.: 0.456 Length: 91
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x A55406 (1-91)

Qy 37 AATATCTTCCACCAATACTCAGTTCCG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 3
A42628
calgranulin B - bovine (fragment)
N;Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory fact
in 2
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997
C;Accession: B22309; A42628
R;Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,
submitted to the Protein Sequence Database, July 1992
A;Reference number: A22309
A;Accession: B22309
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-122 <TAN>
R;Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.
Biochemistry 31, 5898-5905, 1992
A;Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutroph
A;Reference number: A42628; MUID:92304974; PMID:1610833
A;Accession: A42628
A;Molecule type: protein
A;Residues: 4-32,'F',34-56 <DIA>
C;Complex: heterodimer and higher complexes with calgranulin A
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; pho
F;6-40/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>

Alignment Scores:
Pred. No.: 0.448 Length: 122
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x A42628 (1-122)

Qy 37 AATATCTTCCACCAATACTCAGTTCCG 63
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 4
S25281
glTF protein precursor - Escherichia coli (strain K-12)
C;Species: Escherichia coli

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S25281; H65112
R;Castano, I.; Flores, N.; Valle, F.; Covarrubias, A.A.; Bolivar, F.
Mol. Microbiol. 6, 2733-2741, 1992
A;Title: gltF, a member of the gltBDF operon of Escherichia coli, is involved in nitroge
A;Reference number: S25281; MUID:93078627; PMID:1447980
A;Accession: S25281
A;Molecule type: DNA
A;Residues: 1-254 <CAS>
A;Cross-references: UNIPROT:P28721; EMBL:M74162; NID:g146213; PIDN:AAA23909.1; PID:g1462
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H65112
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-254 <BLAT>
A;Cross-references: GB:AE000401; GB:U00096; NID:g1789607; PIDN:AAC76246.1; PID:g1789608;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: gltF
C;Keywords: transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;27-254/Product: gltF protein #status predicted <MAT>
F;213-229/Domain: transmembrane #status predicted <TMM>

Alignment Scores:
Pred. No.: 5.24 Length: 254
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x S25281 (1-254)

QY 254 GCAGCCTTCAGCGCAATGGCTACC 231
|||||
Db 19 AlaAlaPheSerAlaMetAlaThr 26

RESULT 5
D82150
conserved hypothetical protein VC1851 [imported] - Vibrio cholerae (strain N16961 serog
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82150
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82150
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <HEI>
A;Cross-references: UNIPROT:Q9KQ26; GB:AE004260; GB:AE003852; NID:g9656368; PIDN:AAF9499
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1851
A;Map position: 1
C;Superfamily: comB protein

Alignment Scores:
Pred. No.: 5.09 Length: 404
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x D82150 (1-404)

QY 220 TTCATATCCCTGGTAGCCATTGCG 243
|||||
Db 268 PheIleSerLeuValAlaIleAla 275

RESULT 6
G95374
probable ABC transporter, periplasmic solute-binding protein Sma1651 [imported] - Sinorh
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95374
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
. ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: G95374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-525 <KUR>
A;Cross-references: UNIPROT:Q92YH7; GB:AE006469; PIDN:AAK65561.1; PID:g14524039; GSPDB:C
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Sma1651
A;Genome: plasmid

Alignment Scores:
Pred. No.: 5.01 Length: 525
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x G95374 (1-525)

QY 96 CTCACCCCTTAGAGAGGGTGTCAA 73
|||||
Db 96 LeuThrLeuArgGluGlyVallys 103

RESULT 7
T39800
probable DNA-binding protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39800
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21880
A;Accession: T39800
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-900 <MCD>
A;Cross-references: UNIPROT:Q9UUD1; EMBL:AL109731; PIDN:CAB52036.1; GSPDB:GN00067; SPDB
A;Experimental source: strain 972h-; cosmid c19C2
C;Genetics:
A;Gene: SPDB:SPBC19C2.09
A;Map position: 2

Alignment Scores:
Pred. No.: 4.84 Length: 900
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00%		Mismatches: 0
Query Match: 8.79%		Indels: 0
DB: 2		Gaps: 0
US-09-910-208B-12 (1-276) x T39800 (1-900)		
Qy	137 TTGATGGTGTTCGCAAGCTCCTTT 114	
Db	577 LeuMetValPheAlaSerSerPhe 584	
RESULT 8		
S03818		
carboxymethylcellulase (EC 3.2.1.-) precursor - Pseudomonas fluorescens subsp. cellulosa		
C;Species: Pseudomonas fluorescens subsp. cellulosa		
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 04-Apr-2004		
C;Accession: S03818		
R;Hall, J.; Gilbert, H.J.		
Mol. Gen. Genet. 213, 112-117, 1988		
A;Title: The nucleotide sequence of a carboxymethylcellulase gene from Pseudomonas fluorescens subsp. cellulosa		
A;Reference number: S03818; MUID:89127129; PMID:2851699		
A;Accession: S03818		
A;Molecule type: DNA		
A;Residues: 1-962 <HAL>		
A;Cross-references: EMBL:X12570; NID:g45503; PIDN:CAA31082.1; PID:g45504		
A;Note: the authors translated the codon CAG for residue 18 as Gly, ATC for residue 503		
C;Keywords: glycosidase; hydrolase		
F;670-707/Domain: glycosidase GWG domain homology <GWG>		
F;865-962/Domain: bacterial cellulose-binding domain homology <BCB>		
F;866-961/Disulfide bonds: #status predicted		
Alignment Scores:		
Pred. No.:	4.82	Length: 962
Score:	8.00	Matches: 8
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	8.70%	Indels: 0
DB:	2	Gaps: 0
US-09-910-208B-12 (1-276) x S03818 (1-962)		
Qy	18 GCATCTGGAGGAATTGCAATAT 41	
Db	861 AlaSerGlyGlyAsnCysGlnTyr 868	
RESULT 9		
F71350		
hypothetical protein TP0224 - syphilis spirochete		
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)		
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004		
C;Accession: F71350		
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin		
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD		
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.		
Science 281, 375-388, 1998		
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.		
A;Reference number: A71250; MUID:98332770; PMID:9665876		
A;Accession: F71350		
A;Status: preliminary; nucleic acid sequence not shown; translation not shown		
A;Molecule type: DNA		
A;Residues: 1-34 <COL>		
A;Cross-references: UNIPROT:O83253; GB:AE001204; GB:AE000520; NID:g3322492; PIDN:AAC6521		
A;Experimental source: strain Nichols		
C;Genetics:		
A;Gene: TP0224		
Alignment Scores:		
Pred. No.:	72.6	Length: 34
Score:	7.00	Matches: 7
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	7.69%	Indels: 0
DB:	2	Gaps: 0

US-09-910-208B-12 (1-276) x F71350 (1-34)

QY 219 TTCTTGAAAGTCGACCTGTTTC 199
|||||

Db 10 PheLeuLysValAspLeuPhe 16

RESULT 10
B34912
hypothetical protein ftr 5'-region - Methanobacterium thermoautotrophicum (strain Delta
C;Species: Methanobacterium thermoautotrophicum
C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 09-Jul-2004
C;Accession: B34912
R;DiMarco, A.A.; Sment, K.A.; Konisky, J.; Wolfe, R.S.
J. Biol. Chem. 265, 472-476, 1990
A;Title: The formylmethanofuran:tetrahydromethanopterin formyltransferase from Methanob
A;Reference number: A34912; MUID:90094441; PMID:2403564
A;Accession: B34912
A;Molecule type: DNA
A;Residues: 1-50 <DIM>
A;Cross-references: UNIPROT:Q9P994; GB:J05173; NID:g1196490; PIDN:AAA88221.1; PID:g1196
A;Experimental source: strain Delta H
C;Comment: This is the hypothetical translation of a sequence that was not reported as

Alignment Scores:
Pred. No.: 70.9 Length: 50
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x B34912 (1-50)

QY 25 GAGGGAATTGTCAATATCTTC 45
|||||

Db 10 GluGlyIleValAsnIlePhe 16

RESULT 11
S69743
probable membrane protein YPR170c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 26-Aug-1999
C;Accession: S69743; S69742
R;Pauley, A.
submitted to the EMBL Data Library, April 1995
A;Description: The sequence of S. cerevisiae cosmid 9705.
A;Reference number: S59829
A;Accession: S69743
A;Molecule type: DNA
A;Residues: 1-81 <PAU>
A;Cross-references: EMBL:U25842; MIPS:YPR170c
R;Hallsworth, K.
submitted to the EMBL Data Library, April 1995
A;Description: The sequence of S. cerevisiae cosmid 9325.
A;Reference number: S59821
A;Accession: S69742
A;Molecule type: DNA
A;Residues: 82-111 <HAL>
A;Cross-references: EMBL:U25840; MIPS:YPR170c
C;Genetics:
A;Map position: 16R
C;Superfamily: Saccharomyces probable membrane protein YPR170c
C;Keywords: transmembrane protein
F;23-39/Domain: transmembrane #status predicted <TMM>

Alignment Scores:
Pred. No.: 67.5 Length: 111
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.69% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x S69743 (1-111)

QY 131 GTGTTTGCAAGCTCCTTTGTA 111
, |||||
Db 31 ValPheAlaSerSerPheVal 37

RESULT 12
A48418
interleukin-5 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A48418; S37641
R;Uberla, K.; Li, W.Q.; Qin, Z.H.; Richter, G.; Raabe, T.; Diamantstein, T.; Blankenstein
Cytokine 3, 72-81, 1991
A;Title: The rat interleukin-5 gene: characterization and expression by retroviral gene
A;Reference number: A48418; MUID:91355638; PMID:1653053
A;Accession: A48418
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <UBE>
A;Cross-references: UNIPROT:Q08125; EMBL:X54419; NID:g313254; PIDN:CAA38283.1; PID:g3132
A;Experimental source: cell line TR5-1
A;Note: sequence extracted from NCBI backbone (NCBIN:63651, NCBIP:63652)
C;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-132/Product: interleukin-5 #status predicted <MAT>
F;45,74,88/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;61/Disulfide bonds: interchain (to 103) #status predicted
F;103/Disulfide bonds: interchain (to 61) #status predicted

Alignment Scores:
Pred. No.: 66.7 Length: 132
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x A48418 (1-132)

QY 166 GAAATATTCCAAGGCTGGAT 186
|||
Db 64 GluIlePheGlnGlyLeuAsp 70

RESULT 13
ICMS5
interleukin-5 precursor - mouse
N;Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil d
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S00807; A38758; A24898; JS0077; PH0102; B39881
R;Campbell, H.D.; Sanderson, C.J.; Wang, Y.; Hort, Y.; Martinson, M.E.; Tucker, W.Q.J.;
Eur. J. Biochem. 174, 345-352, 1988
A;Title: Isolation, structure and expression of cDNA and genomic clones for murine eosin
n-5.
A;Reference number: S00807; MUID:88254802; PMID:3133208
A;Accession: S00807
A;Molecule type: DNA
A;Residues: 1-133 <CAM>
A;Cross-references: UNIPROT:P04401; EMBL:X06271; NID:g52685; PIDN:CAA29607.1; PID:g52686
A;Accession: A38758
A;Molecule type: mRNA
A;Residues: 1-133 <CAM2>
A;Cross-references: EMBL:X06270; NID:g52687; PIDN:CAA29606.1; PID:g52688
R;Kinashi, T.; Harada, N.; Severinson, E.; Tanabe, T.; Sideras, P.; Konishi, M.; Azuma,
Nature 324, 70-73, 1986
A;Title: Cloning of complementary DNA encoding T-cell replacing factor and identity with
A;Reference number: A24898; MUID:87065032; PMID:3024009
A;Accession: A24898
A;Molecule type: mRNA
A;Residues: 1-133 <KIN>
A;Cross-references: EMBL:X04601; NID:g54898; PIDN:CAA28266.1; PID:g54899

R;Mizuta, T.R.; Tanabe, T.; Nakakubo, H.; Noma, T.; Honjo, T.
Growth Factors 1, 51-57, 1988
A;Title: Molecular cloning and structure of the mouse interleukin-5 gene.
A;Reference number: JS0077; MUID:90180853; PMID:3078564
A;Accession: JS0077
A;Molecule type: DNA
A;Residues: 1-133 <MIZ>
R;Takahashi, T.; Yamaguchi, N.; Mita, S.; Yamaguchi, Y.; Suda, T.; Tominaga, A.; Kikuchi,
Mol. Immunol. 27, 911-920, 1990
A;Title: Structural comparison of murine T-cell (B15IK12)-derived T-cell-replacing facto
A;Reference number: PH0102; MUID:91015093; PMID:2215480
A;Accession: PH0102
A;Molecule type: protein
A;Residues: 21-45,'X',47 <TAK>
R;Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmel
de Vries, J.; Lee, F.D.; Arai, N.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987
A;Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and hum
A;Reference number: A39881; MUID:88041112; PMID:2823259
A;Accession: B39881
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-14,'AA',15-133 <YOK>
C;Genetics:
A;Introns: 47/3; 58/3; 101/3
C;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-133/Product: interleukin-5 #status predicted <MAT>
F;46/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;62/Disulfide bonds: interchain (to 104) #status predicted
F;75,89/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;104/Disulfide bonds: interchain (to 62) #status predicted

Alignment Scores:
Pred. No.: 66.7 Length: 133
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x ICMS5 (1-133)

QY 166 GAAATATTCCAAGGCTGGAT 186
|||
Db 65 GluIlePheGlnGlyLeuAsp 71

RESULT 14
S72253
hemoglobin, extracellular, major globin chain c - Oligobrachia mashikoi
C;Species: Oligobrachia mashikoi
C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: S72253; S72216
R;Yuasa, H.J.; Green, B.N.; Takagi, T.; Suzuki, N.; Vinogradov, S.N.; Suzuki, T.
Biochim. Biophys. Acta 1296, 235-244, 1996
A;Title: Electrospray ionization mass spectrometric composition of the 400 kDa hemoglob.
A;Reference number: S72214; MUID:96409249; PMID:8814231
A;Accession: S72253
A;Molecule type: protein
A;Residues: 1-30 <YUA>
A;Cross-references: UNIPROT:Q7M418
A;Accession: S72216
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 19-147 <YUW>
C;Superfamily: extracellular hemoglobin; globin homology
C;Keywords: chromoprotein; heme; iron; oxygen carrier

Alignment Scores:
Pred. No.: 66.3 Length: 147
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.69% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x S72253 (1-147)

Qy 113 GTAAGCAGCTGCTTCAGCTCA 93

|||||

Db 123 ValSerSerCysPheSerSer 129

RESULT 15

A64476

hypothetical protein MJ1410 - Methanococcus jannaschii

C;Species: Methanococcus jannaschii

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: A64476

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Accession: A64476

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-159 <BUL>

A;Cross-references: UNIPROT:Q58805; GB:U67581; GB:L77117; NID:G2826404; PIDN:AAB99417.1;

C;Genetics:

A;Map position: REV1371312-1370833

Alignment Scores:

Pred. No.: 66 Length: 159
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x A64476 (1-159)

Qy 133 ATCAAGAATATCAAGATAAA 153

|||||

Db 145 IleLysAsnIleLysAspLys 151

Search completed: February 23, 2005, 12:39:07
Job time : 36 secs

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:
      GenCore version 5.1.6
      Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:      February 23, 2005, 12:15:09 ; Search time 115 Seconds
           (without alignments)
           2457.980 Million cell updates/sec

Title:      US-09-910-208B-12
Perfect score: 92
Sequence:    1 atgacaaaacttgaagagca.....attaccacaccacaagag 276

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched:    1612378 seqs, 512079187 residues
Word size:    1
Total number of hits satisfying chosen parameters:    3224408

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPrO_spool_p/HADDAD-09-910208B/runat_23022005_102315_15797/app_query.fasta.1
-DB=UniProt_03 -QFMT=fastan -SUFFIX=oligo.rup -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208B @CGN_1_1_244 @runat_23022005_102315_15797 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :      UniProt_03:*
              1: uniprot_sprot:*
              2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result      No.      Score      Match      Length      DB      ID      Description
-----
1           91      98.9      91         1         S112_HUMAN      P80511 homo sapien
2           9      9.8      70         2         Q9TR16          Q9tr16 bos taurus
3           9      9.8      81         1         S112_RABIT     O77791 oryctolagus
4           9      9.8      91         1         S112_BOVIN     P79105 bos taurus
5           9      9.8      91         1         S112_PIG       P80310 sus scrofa
6           9      9.8      118        1         S109_RABIT     P50117 oryctolagus
7           9      9.8      122        1         S109_BOVIN     P28783 bos taurus
8           9      9.8      402        2         Q6XE66         Q6xe66 uncultured
9           8      8.7      92         1         S106_HORSE     O77691 equus cabal
10          8      8.7      95         2         Q6XG62         Q6xg62 brachydanio
11          8      8.7      175        1         CALB_ASHGO     Q757b7 ashbya goss
12          8      8.7      213        2         Q9H4U1         Q9h4u1 homo sapien
13          8      8.8      248        2         Q87I93         Q87i93 vibrio para
14          8      8.8      254        1         GLTF_ECOLI     P28721 escherichia
15          8      8.8      264        2         Q72V46         Q72v46 leptospira
16          8      8.8      264        2         Q8EZR3         Q8ezr3 leptospira

```

Q6mc24	parachlamyd	311	2	Q6MC24	8.8	8	17	c
Q87tx0	pseudomonas	355	2	Q87TX0	8.7	8	18	c
Q689y0	turnip mosa	362	2	Q689Y0	8.8	8	19	c
Q87qk2	vibrio para	404	2	Q87QK2	8.7	8	20	
Q9kqz6	vibrio chol	404	2	Q9KQZ6	8.7	8	21	
Q8e0n4	streptococc	516	2	Q8E0N4	8.8	8	22	c
Q8e6a8	streptococc	516	2	Q8E6A8	8.8	8	23	c
Q92yh7	rhizobium m	525	2	Q92YH7	8.8	8	24	c
Q8iln4	plasmodium	660	2	Q8ILN4	8.7	8	25	
Q8rvq5	arabidopsis	829	1	SC10_ARATH	8.7	8	26	c
Q7rsl0	plasmodium	869	2	Q7RSL0	8.8	8	27	
Q8t9f2	drosophila	874	2	Q8T9F2	8.7	8	28	
Q9fjl1	arabidopsis	888	2	Q9FJ11	8.8	8	29	c
Q9uud1	schizosacch	900	2	Q9UUD1	8.8	8	30	c
P10476	pseudomonas	962	1	GUNA_PSEFL	8.7	8	31	
Q9vuc2	drosophila	1780	2	Q9VUC2	8.7	8	32	
Q7rix5	plasmodium	1780	2	Q7RIX5	8.7	8	33	
Q7xp84	oryza sativ	1976	2	Q7XPS4	8.8	8	34	c
O83253	treponema p	3331	2	Y224_TREPA	8.8	7	35	c
Q7mey1	vibrio vuln	34	1	Q7MEY1	7.7	7	36	c
Q9p994	methanobact	45	2	Q9P994	7.7	7	37	
Q9gpt5	dictyosteli	50	2	Q9GPT5	7.6	7	38	
Q63e24	bacillus ce	64	2	Q63E24	7.6	7	39	
Q73bf2	bacillus ce	64	2	Q73BF2	7.6	7	40	
Q81g60	bacillus ce	64	2	Q81G60	7.6	7	41	
Q81tb9	bacillus an	64	2	Q81TB9	7.6	7	42	
Q6hlj9	bacillus th	64	2	Q6HLJ9	7.6	7	43	
Q6v5x6	human immu	66	2	Q6V5X6	7.6	7	44	
Q6mpb8	bdellovibri	89	2	Q6MPB8	7.6	7	45	
Q98953	gallus gall	92	1	S106_CHICK	7.6	7	46	
Q8wxg8	homo sapien	98	1	S10Z_HUMAN	7.6	7	47	
Q7y3w6	bacterioph	99	2	Q7Y3W6	7.7	7	48	c
Q6maq3	parachlamyd	102	2	Q6MAQ3	7.6	7	49	
Q88ka6	pseudomonas	104	2	Q88KA6	7.6	7	50	
Q7w021	bordetella	108	2	Q7W021	7.6	7	51	
Q7wcel	bordetella	108	2	Q7WCE1	7.6	7	52	
Q7wqe7	bordetella	108	2	Q7WQE7	7.6	7	53	
Q9s7b3	urtica dioi	112	2	Q9S7B3	7.6	7	54	
Q9syr5	pyrrobaclum	112	2	Q9SYR5	7.6	7	55	
Q8zzp0	acinetobact	119	2	Q8ZZP0	7.6	7	56	
Q6f8r9	acinetobact	120	2	Q6F8R9	7.7	7	57	c
Q9ddw9	xenopus lae	121	2	Q9DDW9	7.7	7	58	c
Q9x4m4	lactobacill	131	2	Q9X4M4	7.6	7	59	
Q62575	meriones un	132	1	IL5_MERUN	7.6	7	60	
Q08125	rattus norv	132	1	IL5_RAT	7.6	7	61	
Q62tm0	bacillus li	132	2	Q62TM0	7.7	7	62	c
Q9r2c9	rattus norv	132	2	Q9R2C9	7.6	7	63	
P04401	mus musculu	133	1	IL5_MOUSE	7.6	7	64	
Q82z63	enterococcu	139	2	Q82Z63	7.7	7	65	c
Q6zu59	homo sapien	143	2	Q6ZU59	7.6	7	66	
Q9qy87	rattus norv	144	2	Q9QY87	7.7	7	67	c
Q7m418	oligobrachi	147	1	GLBC_OLIMA	7.7	7	68	c
Q8bjl3	mus musculu	148	2	Q8BJL3	7.6	7	69	
Q7p4m6	fusobacteri	150	2	Q7P4M6	7.6	7	70	
Q9fpt5	arabidopsis	154	2	Q9FPT5	7.6	7	71	
Q7psx7	anopheles g	157	2	Q7PSX7	7.7	7	72	c
Q6z2k1	oryza sativ	157	2	Q6Z2K1	7.6	7	73	
Q58805	methanococc	159	1	YE10_METJA	7.6	7	74	
Q97vy3	sulfolobus	165	1	LEUD_SULSO	7.6	7	75	
Q88r01	pseudomonas	166	2	Q88R01	7.6	7	76	
Q88ael	pseudomonas	167	2	Q88AE1	7.6	7	77	
Q974q9	sulfolobus	168	1	LEUD_SULTO	7.6	7	78	
Q8g3l2	bifidobacte	168	2	Q8G3L2	7.7	7	79	c
Q8y1w2	ralstonia s	169	2	Q8Y1W2	7.7	7	80	c
Q6n6t6	rhodopseudo	170	2	Q6N6T6	7.6	7	81	
Q6cge6	yarrowia li	173	1	CALB_YARLI	7.6	7	82	
Q957y8	casuarius c	173	2	Q957Y8	7.7	7	83	c
Q9uu93	schizosacch	174	1	CALB_SCHPO	7.6	7	84	
P25296	saccharomyc	174	1	CALB_YEAST	7.6	7	85	
Q6flu4	candida gla	175	1	CALB_CANGA	7.6	7	86	
Q874t7	kluveromyc	175	1	CALB_KLULA	7.6	7	87	
Q7mh50	vibrio vuln	175	2	Q7MH50	7.7	7	88	c
Q9ryc7	deinococcus	177	2	Q9RYC7	7.7	7	89	c

90	7	7.6	182	2	Q62NQ6	Q62nq6 bacillus li	c 163	7	7.7	319	2	Q7NYF2	Q7nyf2 chromobacte
c 91	7	7.7	183	2	Q65194	Q65194 african swi	164	7	7.6	325	2	Q6HGP3	Q6hgp3 bacillus th
c 92	7	7.7	183	2	Q65272	Q65272 african swi	c 165	7	7.7	326	2	Q7VJJ0	Q7vjjo helicobacte
c 93	7	7.7	185	2	Q7QM90	Q7qm90 anopheles g	c 166	7	7.7	326	2	Q8DXV8	Q8dxv8 streptococc
c 94	7	7.7	185	2	Q8EJ16	Q8ej16 shewanella	c 167	7	7.7	326	2	Q8E3H6	Q8e3h6 streptococc
c 95	7	7.7	187	2	Q6URA7	Q6ura7 brachyspira	168	7	7.6	327	2	Q735E8	Q735e8 bacillus ce
c 96	7	7.7	188	2	Q756U6	Q756u6 ashbya goss	169	7	7.6	328	1	PE59_ARATH	Q39034 arabidopsis
c 97	7	7.7	188	2	Q9FJH3	Q9fjh3 arabidopsis	170	7	7.6	334	1	DPOB_HUMAN	P06746 homo sapien
c 98	7	7.6	189	2	Q65D80	Q65d80 bacillus li	171	7	7.6	334	1	DPOB_MOUSE	Q8k409 mus musculu
99	7	7.6	192	2	Q6EBC0	Q6ebc0 trichoplusi	172	7	7.6	334	1	DPOB_RAT	P06766 rattus norv
100	7	7.6	196	2	Q8TNB7	Q8tnb7 methanosarc	173	7	7.6	334	2	Q639D4	Q639d4 bacillus ce
c 101	7	7.7	197	1	YGZ7_YEAST	P53062 saccharomyc	c 174	7	7.7	334	2	Q745H5	Q745h5 mycobacteri
c 102	7	7.6	208	2	Q9EMH3	Q9emh3 amsacta moo	175	7	7.6	334	2	Q9HYL8	Q9hy18 pseudomonas
c 103	7	7.7	217	2	Q7P7B3	Q7p7b3 fusobacteri	176	7	7.6	335	2	Q8XJW3	Q8xjw3 clostridium
c 104	7	7.6	218	2	Q7MWA1	Q7mwa1 porphyromon	177	7	7.6	336	2	Q6BGG5	Q6bgg5 paramecium
c 105	7	7.7	219	2	Q6QVY6	Q6qvy6 pedicularis	178	7	7.6	336	2	Q882R9	Q882r9 pseudomonas
c 106	7	7.6	223	2	Q72XQ2	Q72xq2 bacillus ce	179	7	7.6	336	2	Q8BXK5	Q8bxk5 mus musculu
c 107	7	7.7	225	1	AROM_ECOLI	P08403 escherichia	180	7	7.6	339	2	Q20385	Q20385 rubus hawai
c 108	7	7.7	225	2	Q6QPY1	Q6qpy1 mimulus kel	181	7	7.6	339	2	Q9C6V3	Q9c6v3 arabidopsis
c 109	7	7.7	225	2	Q8FKD8	Q8fk d8 escherichia	c 182	7	7.7	343	2	Q7YFU6	Q7yfu6 manica rubi
c 110	7	7.7	225	2	Q8XEA6	Q8xea6 escherichia	c 183	7	7.7	344	2	Q8VE58	Q8ve58 mus musculu
c 111	7	7.6	226	2	Q8PN66	Q8pn66 xanthomonas	184	7	7.6	345	2	Q9BT58	Q9bt58 homo sapien
c 112	7	7.6	226	2	Q6MRV7	Q6mry7 mycoplasma	185	7	7.6	347	2	Q810Y7	Q810y7 caenorhabdi
c 113	7	7.7	227	2	Q6QPY2	Q6qpy2 leucocarpus	186	7	7.6	350	2	Q22946	Q22946 caenorhabdi
c 114	7	7.7	229	2	Q6UWS1	Q6uws1 homo sapien	187	7	7.6	350	2	Q8T1E2	Q8t1e2 dictyosteli
c 115	7	7.7	229	2	Q9H5X9	Q9h5x9 homo sapien	188	7	7.6	352	2	Q8CNQ8	Q8cnq8 staphylococ
c 116	7	7.7	233	1	NT7_BRARE	Q73797 brachydanio	189	7	7.6	353	2	Q8NVU8	Q8nvu8 staphylococ
c 117	7	7.7	235	2	Q74Z63	Q74z63 ashbya goss	190	7	7.6	353	2	Q99T19	Q99t19 staphylococ
c 118	7	7.6	241	2	Q8PBL1	Q8pbl1 xanthomonas	191	7	7.6	353	2	Q7A4U0	Q7a4u0 staphylococ
c 119	7	7.7	243	2	Q6ZV13	Q6zv13 homo sapien	192	7	7.6	353	2	Q6G874	Q6g874 staphylococ
c 120	7	7.7	247	2	Q8KC40	Q8kc40 chlorobium	193	7	7.6	353	2	Q6GFJ7	Q6gjf7 staphylococ
121	7	7.6	247	2	Q9D015	Q9d015 mus musculu	c 194	7	7.7	354	2	Q7XXQ4	Q7xxq4 oryza sativ
122	7	7.6	259	2	Q9XBG2	Q9xbg2 burkholderi	c 195	7	7.7	355	2	Q65NU4	Q65nu4 bacillus li
c 123	7	7.6	261	2	Q8AA73	Q8aa73 bacteroides	c 196	7	7.7	355	2	Q8UG42	Q8ug42 agrobacteri
124	7	7.6	262	2	Q8GBS6	Q8gbs6 treponema m	c 197	7	7.7	358	2	Q9RYJ0	Q9ryj0 deinococcus
125	7	7.6	266	2	Q98Y57	Q98y57 reptilian p	c 198	7	7.7	362	2	Q689X3	Q689x3 turnip mosa
126	7	7.6	266	2	Q98Y58	Q98y58 reptilian p	199	7	7.6	364	2	Q82E53	Q82e53 streptomyce
127	7	7.6	266	2	Q98Y60	Q98y60 reptilian p	200	7	7.6	365	1	SMS2_HUMAN	Q8nhu3 homo sapien
128	7	7.6	266	2	Q98Y61	Q98y61 reptilian p	201	7	7.6	366	2	Q8UJQ6	Q8ujq6 agrobacteri
129	7	7.6	266	2	Q8A631	Q8a631 bacteroides	202	7	7.6	367	2	Q9X888	Q9x888 streptomyce
130	7	7.6	268	1	LGT_SYNEL	Q8dh03 synecococc	c 203	7	7.7	370	2	Q73PD0	Q73pd0 treponema d
c 131	7	7.6	273	2	Q64PU7	Q64pu7 bacteroides	204	7	7.6	373	1	BIOF_HELPY	Q25320 helicobacte
c 132	7	7.7	274	2	Q8RI36	Q8ri36 fusobacteri	c 205	7	7.7	373	2	Q21149	Q21149 caenorhabdi
c 133	7	7.7	274	2	Q73JE4	Q73je4 treponema d	c 206	7	7.6	375	2	Q8TVP9	Q8tvp9 methanopyru
c 134	7	7.6	276	1	PANC_HELPJ	Q9zn52 helicobacte	207	7	7.6	380	2	Q74DF3	Q74df3 geobacter s
c 135	7	7.7	278	2	Q8GS03	Q8gs03 oryza sativ	208	7	7.6	382	2	Q7D348	Q7d348 agrobacteri
c 136	7	7.7	278	2	Q8FQZ7	Q8fqz7 corynebacte	c 209	7	7.7	383	2	Q97P35	Q97p35 streptococc
c 137	7	7.6	278	2	Q6JE40	Q6je40 humulus jap	c 210	7	7.7	383	2	Q8DNN0	Q8dnn0 streptococc
138	7	7.6	279	2	Q7PTS8	Q7pts8 anopheles g	c 211	7	7.6	386	2	Q8C3H3	Q8c3h3 mus musculu
c 139	7	7.7	282	2	Q9M0T7	Q9m0t7 arabidopsis	c 212	7	7.7	391	2	Q974X7	Q974x7 sulfolobus
c 140	7	7.7	283	2	Q9ALN3	Q9aln3 saccharopol	c 213	7	7.7	395	2	Q891R0	Q891r0 clostridium
c 141	7	7.6	288	2	Q7RV11	Q7rv11 neurospora	c 214	7	7.6	396	2	Q75824	Q75824 homo sapien
c 142	7	7.7	288	2	Q7VHG2	Q7vhg2 helicobacte	c 215	7	7.7	396	2	Q8DLV1	Q8dly1 synecococc
c 143	7	7.7	292	2	Q6IEX5	Q6iex5 homo sapien	c 216	7	7.6	401	2	Q6BUL5	Q6bul5 debaryomyce
c 144	7	7.7	293	1	XT31_ARATH	P93046 arabidopsis	c 217	7	7.7	401	2	Q9NT09	Q9nt09 homo sapien
c 145	7	7.7	293	2	Q8LYV8	Q8lyv8 polytomella	c 218	7	7.6	402	2	Q86VW6	Q86vw6 homo sapien
c 146	7	7.6	293	2	Q9D140	Q9d140 mus musculu	219	7	7.6	409	1	MNTH_YERPE	Q8zck2 yersinia pe
c 147	7	7.7	294	2	Q6N476	Q6n476 rhodopsuendo	220	7	7.6	409	2	Q668N2	Q668n2 yersinia ps
c 148	7	7.6	299	2	Q8Z086	Q8z086 anabaena sp	c 221	7	7.7	411	2	Q82VF8	Q82vf8 nitrosomona
c 149	7	7.6	300	2	Q755Z4	Q755z4 ashbya goss	c 222	7	7.7	413	2	Q8EFQ2	Q8efq2 shewanella
c 150	7	7.7	303	1	PCPR_SPHCR	P52679 sphingobium	c 223	7	7.6	415	2	Q6P5L8	Q6p5l8 brachydanio
c 151	7	7.7	305	2	Q8N308	Q8n308 homo sapien	224	7	7.6	417	2	Q66KC4	Q66kc4 xenopus tro
c 152	7	7.7	305	2	Q8N7C7	Q8n7c7 homo sapien	225	7	7.6	417	2	Q6PAY8	Q6pay8 xenopus lae
c 153	7	7.6	307	2	P94333	P94333 bradyrhizob	c 226	7	7.6	418	2	Q6YN16	Q6yn16 homo sapien
c 154	7	7.6	308	2	Q8RGK4	Q8rgk4 fusobacteri	227	7	7.7	419	2	Q7PTX3	Q7ptx3 anopheles g
c 155	7	7.6	310	1	PANE_AQUAE	Q67619 aquifex aeo	c 228	7	7.6	421	2	Q895H9	Q895h9 clostridium
c 156	7	7.7	315	1	YAI4_HAEIN	P44094 haemophilus	229	7	7.6	421	2	Q6P8L5	Q6p8l5 mus musculu
c 157	7	7.7	315	2	Q9CL82	Q9cl82 pasteurella	c 230	7	7.7	427	2	Q8TNR5	Q8tnr5 methanosarc
c 158	7	7.7	316	2	Q8CGR1	Q8cgr1 mus musculu	c 231	7	7.7	430	2	Q9ULP6	Q9ulp6 homo sapien
c 159	7	7.7	316	2	Q9D3V4	Q9d3v4 mus musculu	c 232	7	7.7	431	2	Q84G45	Q84g45 rhizobium l
c 160	7	7.7	318	1	Q4HC_HUMAN	Q8ng74 homo sapien	c 233	7	7.6	434	2	Q8BMC7	Q8bmc7 mus musculu
c 161	7	7.6	318	2	Q9KM43	Q9km43 vibrio chol	234	7	7.6	438	2	Q96UT4	Q96ut4 emericeila
c 162	7	7.7	319	2	Q9HS11	Q9hs11 halobacteri	235	7	7.6	438	2	Q735V8	Q735v8 bacillus ce

236	7	7.6	442	2	Q20755	Q20755 caenorhabdi	309	7	7.6	631	2	Q6MSS3	Q6mss3 mycoplasma
c 237	7	7.7	443	2	Q7MA91	Q7ma91 wolinnella s	c 310	7	7.7	638	2	Q75GM0	Q75gm0 oryza sativ
c 238	7	7.7	443	2	Q8UCI2	Q8uci2 agrobacteri	311	7	7.6	639	2	Q7SON7	Q7son7 neurospora
239	7	7.6	447	1	GASR_HUMAN	P32239 homo sapien	312	7	7.6	641	2	Q9H6W3	Q9h6w3 homo sapien
240	7	7.6	447	2	Q16144	Q16144 homo sapien	313	7	7.6	641	2	Q7QU29	Q7qu29 giardia lam
241	7	7.6	447	2	Q92492	Q92492 homo sapien	314	7	7.6	643	2	Q7PPE7	Q7ppe7 anopheles g
242	7	7.6	452	1	GASR_RABIT	P46627 oryctolagus	315	7	7.6	643	2	Q9Z6G3	Q9z6g3 vibrio para
243	7	7.6	453	1	GASR_CANFA	P30552 canis famil	316	7	7.6	643	2	Q87MJ8	Q87mj8 oceanobacil
244	7	7.6	454	1	GASR_BOVIN	P79266 bos taurus	317	7	7.6	650	2	Q8EP63	Q8ep63 apteronotus
c 245	7	7.7	458	2	Q60957	O60957 leishmania	c 318	7	7.7	651	2	Q9DDN7	Q9ddn7 treponema d
c 246	7	7.7	458	2	Q9PNA3	Q9pna3 campylobact	319	7	7.6	656	2	Q73RI8	Q73ri8 helicobacte
c 247	7	7.7	459	2	Q80WT9	Q80wt9 mus musculu	320	7	7.6	660	2	Q6PRE6	Q6pre6 geobacter s
c 248	7	7.7	460	2	Q6F1J3	Q6f1j3 mesoplasma	c 321	7	7.7	662	2	Q74CW0	Q74cw0 xenopus lae
249	7	7.6	465	2	Q9LZD8	Q9lzd8 arabidopsis	c 322	7	7.7	662	2	Q6DJL3	Q6dlj3 oceanobacil
c 250	7	7.7	469	2	Q96HN8	Q96hn8 homo sapien	c 323	7	7.7	667	2	Q8ELZ9	Q8elz9 bradyrhizob
c 251	7	7.7	469	2	Q9NVE1	Q9nvel homo sapien	c 324	7	7.7	676	2	Q89HT3	Q89ht3 deinococcus
c 252	7	7.7	469	2	Q6Z4S6	Q6z4s6 oryza sativ	c 325	7	7.7	678	2	Q9RTM4	Q9rtm4 dictyosteli
253	7	7.6	470	2	Q04679	O04679 lycopersico	326	7	7.6	682	2	Q9GPR8	Q9gpr8 oceanobacil
254	7	7.6	470	2	P93228	P93228 lycopersico	327	7	7.6	683	2	Q8CXE4	Q8cxe4 caedibacter
255	7	7.6	476	2	Q7SXD7	Q7sxd7 brachydanio	c 328	7	7.7	701	2	Q6TFH1	Q6tfh1 xanthomonas
256	7	7.6	478	2	Q83920	Q83920 treponema p	c 329	7	7.6	704	2	Q8P7W7	Q8p7w7 candida gla
257	7	7.6	481	2	Q9BZC0	Q9bzc0 homo sapien	c 330	7	7.7	711	2	Q6FQB4	Q6fqb4 symbiobacte
258	7	7.6	481	2	Q7KFF8	Q7kff8 drosophila	c 331	7	7.7	712	2	Q67KG5	Q67kg5 shewanella
259	7	7.6	482	1	VGLY_TACV7	P31842 tacaribe vi	332	7	7.6	712	2	Q8EF46	Q8ef46 homo sapien
260	7	7.6	483	1	VGLY_TACV5	P31841 tacaribe vi	333	7	7.6	718	1	HOK3_HUMAN	Q86v88 mus musculu
261	7	7.6	483	1	VGLY_TACVT	P31840 tacaribe vi	334	7	7.6	718	1	HOK3_MOUSE	Q86v88 mus musculu
262	7	7.6	483	2	Q8Y7T3	Q8y7t3 listeria mo	335	7	7.6	719	2	Q6GQ73	Q6gq73 xenopus lae
c 263	7	7.7	484	2	Q9NVU9	Q9nvu9 homo sapien	336	7	7.6	721	2	Q6NRB0	Q6nrb0 xenopus lae
c 264	7	7.7	484	2	Q6VMT3	Q6vmt3 myxococcus	337	7	7.6	722	2	Q7X5J8	Q7x5j8 leuconostoc
265	7	7.6	485	2	Q8N6W0	Q8n6w0 homo sapien	c 338	7	7.7	723	2	Q7Z402	Q7z402 homo sapien
266	7	7.6	485	2	Q8SZ35	Q8sz35 drosophila	c 339	7	7.7	723	2	Q7Z5M4	Q7z5m4 homo sapien
267	7	7.6	485	2	Q9VNM1	Q9vnm1 drosophila	c 340	7	7.7	723	2	Q86WX0	Q86wx0 homo sapien
c 268	7	7.7	487	2	Q969J4	Q969j4 homo sapien	c 341	7	7.7	731	1	CND2_MOUSE	Q8ci56 mus musculu
c 269	7	7.7	489	2	Q96BY8	Q96by8 homo sapien	342	7	7.6	733	2	Q9DYB8	Q9dyb8 tt virus. h
c 270	7	7.7	489	2	Q6UX01	Q6ux01 homo sapien	343	7	7.6	739	2	Q8TWW7	Q8tww7 methanopyru
271	7	7.6	492	2	Q9EX69	Q9ex69 alcaligenes	c 344	7	7.7	747	2	Q8S9Y3	Q8s9y3 arabidopsis
272	7	7.6	495	1	VGLY_TACV	P18141 tacaribe vi	345	7	7.6	758	2	Q7UIV4	Q7uiv4 rhodopirell
273	7	7.6	496	2	Q99LV2	Q99lv2 mus musculu	c 346	7	7.7	768	2	Q8EUF9	Q8euf9 mycoplasma
c 274	7	7.7	506	2	Q630V8	Q630v8 bacillus ce	347	7	7.6	770	2	Q60999	Q60999 dictyosteli
c 275	7	7.7	506	2	Q72XG3	Q72xg3 bacillus ce	348	7	7.6	784	2	Q7N0L5	Q7n0l5 photorhabdu
c 276	7	7.7	506	2	Q81K10	Q81k10 bacillus an	349	7	7.6	793	2	Q8KAF7	Q8kaf7 chlorobium
c 277	7	7.7	506	2	Q6HAZ5	Q6haz5 bacillus th	350	7	7.6	821	2	Q8IC16	Q8ic16 plasmodium
c 278	7	7.6	508	2	Q6DFS1	Q6dfs1 xenopus tro	c 351	7	7.7	822	2	Q7P9M6	Q7p9m6 rickettsia
c 279	7	7.7	509	2	Q9SVM2	Q9svm2 arabidopsis	c 352	7	7.7	822	2	Q92GK9	Q92gk9 rickettsia
280	7	7.6	516	2	Q96LC6	Q96lc6 homo sapien	353	7	7.6	827	2	Q6H8R9	Q6h8r9 ustilago ma
281	7	7.6	516	2	Q9NYK7	Q9nyk7 homo sapien	354	7	7.6	839	2	Q74B54	Q74b54 geobacter s
c 282	7	7.7	517	2	Q672X2	Q672x2 corymborkis	c 355	7	7.7	842	1	EF2_PICPA	Q874b9 pichia past
c 283	7	7.6	522	1	IMA2_XENLA	P52171 xenopus lae	c 356	7	7.7	842	1	EF2_SCHPO	O14460 schizosacch
c 284	7	7.7	523	2	Q07904	Q07904 saccharomyc	c 357	7	7.7	842	2	Q6CI99	Q6ci99 yarrowia li
285	7	7.6	523	2	Q8EVI4	Q8evy4 mycoplasma	c 358	7	7.7	844	1	EF2_NEUCR	Q96x45 neurospora
c 286	7	7.7	529	2	Q65CB5	Q65cb5 streptomyce	c 359	7	7.7	845	2	Q6AVG4	Q6avg4 oryza sativ
c 287	7	7.7	530	2	Q751C5	Q751c5 ashbya goss	c 360	7	7.6	845	2	Q7VSQ4	Q7vsq4 bordetella
288	7	7.6	530	2	Q6KBZ2	Q6kbz2 alicyclobac	c 361	7	7.7	869	2	O23253	O23253 arabidopsis
289	7	7.6	530	2	Q8KD27	Q8kd27 chlorobium	362	7	7.6	870	2	Q7W363	Q7w363 bordetella
c 290	7	7.7	542	2	Q9ZBG2	Q9zb92 streptomyce	363	7	7.6	870	2	Q7WEI0	Q7wei0 bordetella
c 291	7	7.7	549	1	YJCE_ECOLI	P32703 escherichia	c 364	7	7.7	881	2	Q88FU9	Q88fu9 pseudomonas
c 292	7	7.7	549	2	Q7A924	Q7a924 escherichia	365	7	7.6	882	2	Q8BL87	Q8bli87 mus musculu
c 293	7	7.7	549	2	Q8X5U0	Q8x5u0 escherichia	366	7	7.6	889	2	Q8BUI9	Q8bui9 mus musculu
c 294	7	7.7	549	2	Q8FAZ5	Q8faz5 escherichia	c 367	7	7.7	891	2	Q93YT3	Q93yt3 arabidopsis
c 295	7	7.7	549	2	Q83IR1	Q83ir1 shigella fl	c 368	7	7.7	931	2	Q882J5	Q882j5 pseudomonas
c 296	7	7.7	550	2	Q980I2	Q980i2 sulfolobus	c 369	7	7.7	942	2	Q6CVL6	Q6cvl6 kluyveromyc
c 297	7	7.7	556	2	Q7RI98	Q7ri98 plasmodium	370	7	7.6	959	2	Q6NBB4	Q6nbb4 rhodopseudo
c 298	7	7.7	571	2	P78802	P78802 schizosacch	371	7	7.6	981	2	Q75H66	Q75h66 oryza sativ
c 299	7	7.6	578	2	Q822I0	Q822i0 chlamydomphi	372	7	7.6	1010	2	Q76BE3	Q76be3 amia calva
c 300	7	7.7	581	2	Q98HN2	Q98hn2 rhizobium l	373	7	7.6	1030	2	Q875U4	Q875u4 saccharomyc
301	7	7.6	585	2	Q9BHK6	Q9bhk6 spraguehea lo	374	7	7.6	1051	2	Q24007	Q24007 drosophila
302	7	7.6	587	2	Q6Y7R8	Q6y7r8 staphylococ	375	7	7.6	1051	2	Q95PA9	Q95pa9 drosophila
303	7	7.6	588	2	Q7NCV8	Q7ncv8 gloeobacter	c 376	7	7.7	1055	2	Q6P0M4	Q6p0m4 homo sapien
c 304	7	7.7	593	2	Q92P44	Q92p44 rhizobium m	377	7	7.6	1059	2	Q7YN57	Q7yn57 eimeria ten
305	7	7.6	594	2	Q8RY19	Q8ry19 arabidopsis	378	7	7.6	1076	2	Q8MLT4	Q8mlt4 drosophila
306	7	7.6	601	2	P73278	P73278 synechocyst	379	7	7.6	1076	2	Q6AWQ3	Q6awq3 drosophila
c 307	7	7.7	605	2	Q75J23	Q75j23 oryza sativ	380	7	7.6	1083	2	Q48839	Q48839 arabidopsis
308	7	7.6	614	2	Q7P5F5	Q7p5f5 fusobacteri	381	7	7.6	1088	2	Q6ZUM6	Q6zum6 homo sapien

382	7	7.6	1123	1	SYLC NEUCR	P10857 neurospora	C 455	6	6.6	60	2	Q7Y3P4	Q7Y3P4 enterobacte
383	7	7.6	1130	1	SBCC_BACSU	O06714 bacillus su	456	6	6.5	60	2	Q55092	Q55092 synechocyst
384	7	7.6	1135	2	Q84W49	Q84W49 arabidopsis	C 457	6	6.6	61	2	Q8UHF3	Q8UHF3 agrobacteri
385	7	7.7	1152	2	Q7Z355	Q7Z355 homo sapien	458	6	6.5	61	2	Q81Z37	Q81Z37 bacillus an
386	7	7.6	1154	2	Q6K685	Q6K685 oryza sativ	459	6	6.5	62	2	Q72MN5	Q72MN5 leptospira
387	7	7.7	1157	2	Q94525	Q94525 schizosacch	460	6	6.5	62	2	Q8CLAB	Q8CLAB yersinia pe
388	7	7.6	1188	2	Q9KA07	Q9KA07 bacillus ha	461	6	6.5	65	2	Q8XEW5	Q8XEW5 salmonella
389	7	7.6	1192	2	Q9S7T0	Q9S7T0 arabidopsis	462	6	6.5	65	2	Q7CQZ8	Q7CQZ8 salmonella
390	7	7.6	1231	2	Q97140	Q97140 dictyosteli	C 463	6	6.6	67	2	Q61293	Q61293 anthocidari
391	7	7.6	1239	1	Y478 HUMAN	Q9NUA8 homo sapien	464	6	6.5	67	2	Q6MDM7	Q6MDM7 parachlamyd
392	7	7.7	1242	2	Q7Z3U5	Q7Z3U5 homo sapien	C 465	6	6.6	68	2	Q649X8	Q649X8 uncultured
393	7	7.7	1262	2	Q7Z3T4	Q8BU30 mus musculu	C 466	6	6.6	68	2	Q991L0	Q991L0 hepatitis b
394	7	7.7	1262	2	Q6NXX4	Q7Z3T4 homo sapien	C 467	6	6.6	69	2	Q9MP09	Q9MP09 forelius ch
395	7	7.7	1262	2	Q6NXX4	Q6NXX4 mus musculu	C 468	6	6.6	69	2	Q64JX4	Q64JX4 plagiolepis
396	7	7.7	1266	1	SYI HUMAN	P41252 homo sapien	C 469	6	6.6	69	2	Q64JY2	Q64JY2 myrmecocyst
397	7	7.7	1271	2	Q6PGU7	Q6PGU7 brachydanio	C 470	6	6.6	69	2	Q64JY4	Q64JY4 lasius psam
398	7	7.6	1307	2	Q62A85	Q62A85 burkholderi	C 471	6	6.6	69	2	Q64JY6	Q64JY6 lasius pall
399	7	7.6	1319	2	Q63NS2	Q63NS2 burkholderi	C 472	6	6.6	69	2	Q64JY8	Q64JY8 lasius nige
400	7	7.6	1335	2	Q00886	Q00886 dictyosteli	C 473	6	6.6	69	2	Q64JZ0	Q64JZ0 lasius emar
401	7	7.6	1366	1	RPC2 PROMP	Q7V008 prochloroco	C 474	6	6.6	69	2	Q64JZ2	Q64JZ2 lasius brun
402	7	7.6	1419	2	Q8I3G5	Q8I3G5 plasmodium	C 475	6	6.6	69	2	Q64JZ4	Q64JZ4 lasius alie
403	7	7.6	1450	2	Q9LFF0	Q9LFF0 arabidopsis	C 476	6	6.6	69	2	Q64K06	Q64K06 lasius flav
404	7	7.6	1504	2	Q9ZGA6	Q9ZGA6 streptomyce	C 477	6	6.5	69	2	Q74ES1	Q74ES1 geobacter s
405	7	7.6	1539	2	Q7R2Y4	Q7R2Y4 giardia lam	478	6	6.5	69	2	Q9PIU4	Q9PIU4 campylobact
406	7	7.6	1580	2	Q754A4	Q754A4 ashbya goss	C 479	6	6.6	69	2	Q64JZ6	Q64JZ6 lasius umbr
407	7	7.7	1647	2	P78847	P78847 schizosacch	C 480	6	6.6	70	2	Q64JZ8	Q64JZ8 lasius jens
408	7	7.7	1674	2	Q9FVU8	Q9FVU8 arabidopsis	C 481	6	6.6	70	2	Q64K00	Q64K00 lasius dist
409	7	7.7	1893	2	Q7S1Z7	Q7S1Z7 neurospora	C 482	6	6.6	70	2	Q64K02	Q64K02 lasius meri
410	7	7.6	1906	1	DICE MOUSE	Q8R418 mus musculu	C 483	6	6.6	70	2	Q64K04	Q64K04 lasius fuli
411	7	7.6	1944	2	Q6E0X2	Q6E0X2 maize fine	C 484	6	6.6	70	2	Q64K08	Q64K08 acanthomyop
412	7	7.6	1964	2	Q8RUA5	Q8RUA5 oryza sativ	C 485	6	6.5	70	2	Q6PVH5	Q6PVH5 pseudomonas
413	7	7.6	1964	2	Q9M658	Q9M658 arabidopsis	C 486	6	6.6	71	2	Q9X5W8	Q9X5W8 pantoea cit
414	7	7.6	2001	2	Q9M659	Q9M659 arabidopsis	C 487	6	6.6	71	2	Q9YRP7	Q9YRP7 human immun
415	7	7.6	2001	2	Q09705	Q09705 lassa virus	C 488	6	6.5	72	2	Q8UF17	Q8UF17 agrobacteri
416	7	7.6	2219	2	Q6GWR8	Q6GWR8 lassa virus	C 489	6	6.6	73	1	VE5 HPV18	P06792 human papil
417	7	7.6	2219	2	Q6GWS6	Q6GWS6 lassa virus	C 490	6	6.5	74	2	P94555	P94555 bacillus su
418	7	7.6	2220	2	Q6GWS2	Q6GWS2 lassa virus	491	6	6.5	74	2	Q8EPJ2	Q8EPJ2 oceanobacil
419	7	7.6	2220	2	Q6Y630	Q6Y630 lassa virus	C 492	6	6.6	75	2	Q6L1Q3	Q6L1Q3 picrophilus
420	7	7.6	2254	2	Q9LN02	Q9LN02 arabidopsis	C 493	6	6.5	75	2	Q8X293	Q8X293 escherichia
421	7	7.7	2959	2	Q7RJV1	Q7RJV1 plasmodium	C 494	6	6.6	75	2	Q737P7	Q737P7 bacillus ce
422	7	7.6	3364	2	Q8IM60	Q8IM60 plasmodium	C 495	6	6.6	76	2	Q9DEX4	Q9DEX4 gallus gall
423	7	7.6	3377	2	Q8IEH5	Q8IEH5 plasmodium	C 496	6	6.5	77	2	Q7V1X6	Q7V1X6 prochloroco
424	7	7.6	3985	2	Q7RIW0	Q7RIW0 plasmodium	C 497	6	6.6	77	2	Q8VBD6	Q8VBD6 white spot
425	7	7.6	4306	2	Q9JJ79	Q9JJ79 rattus norv	C 498	6	6.5	78	1	XP1 XENLA	Q00222 xenopus lae
426	7	7.7	4594	2	Q6YJK2	Q6YJK2 strongyloce	C 499	6	6.6	78	2	Q94G67	Q94G67 amaranthus
427	7	7.7	4696	2	Q6CFC5	Q6CFC5 yarrowia li	500	6	6.5	78	2	P70713	P70713 rattus norv
428	6	6.5	28	2	Q9BM69	Q9BM69 aphid sp. i							
429	6	6.5	28	2	Q86528	Q86528 grapevine f							
430	6	6.5	30	2	Q9MJF6	Q9MJF6 candida alb							
431	6	6.6	33	2	Q8EBD6	Q8EBD6 shewanella							
432	6	6.6	35	2	Q50884	Q50884 borrelia bu							
433	6	6.5	40	2	Q95Z13	Q95Z13 ceratitis r							
434	6	6.6	41	2	Q91F85	Q91F85 chilo iride							
435	6	6.6	42	2	Q6TA42	Q6TA42 schistosoma							
436	6	6.6	45	2	Q8X215	Q8X215 escherichia							
437	6	6.6	45	2	Q9PFS9	Q9PFS9 xylella fas							
438	6	6.5	46	1	DEGQ_BACLI	P12051 bacillus li							
439	6	6.6	46	2	Q6I6D1	Q6I6D1 escherichia							
440	6	6.5	46	2	Q65FH3	Q65FH3 bacillus li							
441	6	6.6	47	2	Q7QUU1	Q7QUU1 giardia lam							
442	6	6.6	47	2	Q7LZD6	Q7LZD6 oncorhynch							
443	6	6.6	50	2	Q742A9	Q742A9 mycobacteri							
444	6	6.5	52	2	Q64RS8	Q64RS8 bacteroides							
445	6	6.5	52	2	Q98809	Q98809 yam mosaic							
446	6	6.6	53	2	Q7RBD8	Q7RBD8 plasmodium							
447	6	6.6	55	2	Q94SJ0	Q94SJ0 antigon							
448	6	6.6	57	2	Q64220	Q64220 rattus sp.							
449	6	6.6	58	2	Q7R0D1	Q7R0D1 giardia lam							
450	6	6.5	58	2	Q6ZHL0	Q6ZHL0 oryza sativ							
451	6	6.5	58	2	Q7P6Y5	Q7P6Y5 fusobacteri							
452	6	6.5	59	1	Y586 PYRAE	Q8ZSL3 pyrobaculum							
453	6	6.6	59	2	Q9YE39	Q9YE39 aeropyrum p							
454	6	6.6	59	2	Q6UUL6	Q6UUL6 oryza sativ							

ALIGNMENTS

RESULT 1
S112_HUMAN STANDARD; PRT; 91 AA.
ID S112_HUMAN STANDARD; PRT; 91 AA.
AC P80511; P83219;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Calgranulin C (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding protein in amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].
GN Name=S100A12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1;
RA Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;
RT "Characterization of the human S100A12 (calgranulin C, p6, CAAF1, CGRP) gene, a new member of the S100 gene cluster on chromosome 1q21.";
RL Cell Calcium 20:459-464(1996).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=96192053; PubMed=8619860; DOI=10.1006/bbrc.1996.0600;
RA Yamamura T.; Hitomi J., Nagasaki K., Suzuki M., Takahashi E.,
RA Saito S., Takada T., Yamaguchi K.;
RT "Human CAAF1 gene -- molecular cloning, gene structure, and chromosome
RT mapping.";
RL Biochem. Biophys. Res. Commun. 221:356-360(1996).
RN [3]
RP SEQUENCE.
RX MEDLINE=96192069; PubMed=8619876; DOI=10.1006/bbrc.1996.0616;
RA Marti T., Erttmann K.D., Gallin M.Y.;
RT "Host-parasite interaction in human onchocerciasis: identification and
RT sequence analysis of a novel human calgranulin.";
RL Biochem. Biophys. Res. Commun. 221:454-458(1996).
RN [4]
RP SEQUENCE.
RC TISSUE=Neutrophils;
RX MEDLINE=96332419; PubMed=8769108; DOI=10.1006/bbrc.1996.1144;
RA Ilg E.C., Troxler H., Buerigisser D.M., Kuster T., Markert M.,
RA Guignard F., Hunziker P., Birchler N., Heizmann C.W.;
RT "Amino acid sequence determination of human S100A12 (P6, calgranulin
RT C, CGRP, CAAF1) by tandem mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
RN [5]
RP SEQUENCE OF 1-20.
RX MEDLINE=95351965; PubMed=7626002;
RA Guignard F., Maue J., Markert M.;
RT "Identification and characterization of a novel human neutrophil
RT protein related to the S100 family.";
RL Biochem. J. 309:395-401(1995).
RN [6]
RP SEQUENCE OF '77-91, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY.
RC TISSUE=Nasal mucus;
RX MEDLINE=21413725; PubMed=11522286; DOI=10.1016/S0014-5793(01)02731-4;
RA Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;
RT "Calcitermin, a novel antimicrobial peptide isolated from human airway
RT secretions.";
RL FEBS Lett. 504:5-10(2001).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
RX MEDLINE=21065388; PubMed=11134923; DOI=10.1107/S090744490001458X;
RA Moroz O.V., Antson A.A., Murshudov G.N., Maitland N.J., Dodson G.G.,
RA Wilson K.S., Skibshoj I., Lukanidin E.M., Bronstein I.B.;
RT "The three-dimensional structure of human S100A12.";
RL Acta Crystallogr. D 57:20-29(2001).
CC -!- FUNCTION: Calcitermin possesses antifungal activity against
CC C.albicans and is also active against E.coli and P.aeruginosa but
CC not L.monocytogenes and S.aureus.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: Monocytes and lymphocytes.
CC -!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=1-91;
CC NOTE=Ref.6.
CC -!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=77-91;
CC NOTE=Ref.6.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
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CC -----
DR EMBL; X97859; CAA66453.1; -.
DR EMBL; X98288; CAA66934.1; -.
DR EMBL; X98289; CAA66934.1; JOINED.
DR EMBL; X98290; CAA66934.1; JOINED.
DR EMBL; X98289; CAB94792.1; -.
DR EMBL; X98290; CAB94792.1; JOINED.
DR EMBL; D49549; BAA08497.1; -.
DR EMBL; D83664; BAA12036.1; -.

DR EMBL; D83657; BAA12030.1; -.
DR PIR; JC4712; JC4712.
DR PDB; 1B8A; X-ray; A/B=1-91.
DR PDB; 1GQM; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-91.
DR PDB; 1ODB; X-ray; A/B/C/D/E/F=1-91.
DR Genew; HGNC:10489; S100A12.
DR MIM; 603112; -.
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0005626; C:insoluble fraction; TAS.
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW 3D-structure; Antibiotic; Calcium-binding; Direct protein sequencing;
KW Fungicide; Metal-binding; Zinc.
FT INIT_MET 0 0
FT PEPTIDE 77 91 Calcitermin.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
FT HELIX 2 18
FT TURN 19 19
FT TURN 24 25
FT STRAND 26 27
FT HELIX 29 39
FT TURN 41 43
FT TURN 45 48
FT HELIX 50 60
FT TURN 62 63
FT STRAND 68 69
FT HELIX 70 85
SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;

Alignment Scores:
Pred. No.: 2,47e-84 Length: 91
Score: 91.00 Matches: 91
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.91% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S112_HUMAN (1-91)

QY 4 ACAAACCTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCGG 63
|||||
Db 1 ThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerValArg 20

QY 64 AAGGGGCATTTTGACACCCTCTCTAAGGGTGAGCTGAAGCAGCTGTCTACAAAGGAGCTT 123
|||||
Db 21 LysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGluLeu 40

QY 124 GCAACACCATCAAGAATATCAAAGATAAAGCTGTCAATTGATGAATATTTCCAAGGCCTG 183
|||||
Db 41 AlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60

QY 184 GATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAATTATATCCCTGGTAGCCATTGCG 243
|||||
Db 61 AspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80

QY 244 CTGAAGGCTGCCATTACCACACCCACAAAGAG 276
|||||
Db 81 LeuLysAlaAlaHisTyrHisThrHisLysGlu 91

RESULT 2
Q9TR16
ID Q9TR16 PRELIMINARY; PRT; 70 AA.
AC Q9TR16;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DR EMBL; D49548; BAA08496.1; --
DR EMBL; AF011757; AAB65423.1; --
DR HSSP; P80511; 1GQM.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Metal-binding; Zinc.
FT INIT MET 0 0 By similarity.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

Alignment Scores:
Pred. No.: 5.9 Length: 91
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S112_BOVIN (1-91)
QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
|||||
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 5
S112_PIG
ID S112_PIG STANDARD; PRT; 91 AA.
AC P80310;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC).
GN Name=S100A12;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC TISSUE=Granulocyte; PubMed=7961855;
RX MEDLINE=95050708; PubMed=7961855;
RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
RT "Primary structure and binding properties of calgranulin C, a novel
RT S100-like calcium-binding protein from pig granulocytes.";
RL J. Biol. Chem. 269:28929-28936(1994).
CC -!- TISSUE SPECIFICITY: Found essentially in granulocytes with small
CC amounts found in lymphocytes.
CC -!- MISCELLANEOUS: In the absence of zinc binds one calcium ion per
CC molecule, in the presence of zinc binds two calcium ions per
CC molecule.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
DR PIR; A55406; A55406.
DR HSSP; P80511; 1E8A.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Direct protein sequencing; Metal-binding; Zinc.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 91 AA; 10614 MW; B4204461432D7FCE CRC64;

Alignment Scores:
Pred. No.: 5.9 Length: 91
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S112_PIG (1-91)
QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
|||||
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 6
S109_RABIT
ID S109_RABIT STANDARD; PRT; 118 AA.
AC P50117;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin B (Migration inhibitory factor-related protein 14) (MRP-
DE 14) (Fragment).
GN Name=S100A9; Synonyms=MRP-14;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Neutrophils;
RX MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
RA Yang Z., de Veer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
RA Underwood J.R., Robinson H.C.;
RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
RT calgranulin C when incubated with inorganic [35S]sulfate.";
RL J. Biol. Chem. 271:19802-19809(1996).
RN [2]
RP SEQUENCE OF 45-82 FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=94198229; PubMed=8148323;
RA Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
RT "Dynamic changes in mRNA expression of neutrophils during the course
RT of acute inflammation in rabbits.";
RL Int. Immunol. 6:149-156(1994).
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
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CC -----
DR EMBL; AF091849; AAC61771.1; --
DR EMBL; D17404; BAA04227.1; --
DR PIR; I46861; I46861.
DR HSSP; P06702; 1IRJ.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Repeat.
FT NON_TER 1 1
FT CA_BIND 9 22 EF-hand 1; low affinity (Potential).
FT CA_BIND 53 64 EF-hand 2; high affinity (Potential).
FT

```
FT DOMAIN 103 118 2 X 8 AA tandem repeats of G-H-G-H-G-H-S-
FT REPEAT 103 110 H.
FT REPEAT 111 118 1.
SQ SEQUENCE 118 AA; 13292 MW; 7496118E21AD5C41 CRC64;

Alignment Scores:
Pred. No.: 5.66 Length: 118
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S109_RABIT (1-118)
QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
| | | | | | | | | | | | | | | | | | | | | |
Db 3 AsnilePheHisGlnTyrSerValArg 11

RESULT 7
S109_BOVIN
ID S109_BOVIN STANDARD; PRT; 122 AA.
AC P28783;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin B (Neutrophil cytosolic 23 kDa protein) (P23) (BEE22)
DE (Fragment).
GN Name=S100A9;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Oesophageal epithelium;
RX MEDLINE=93280230; PubMed=8505358;
RA Tang T.K., Hong T.-M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-J.,
RA Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.J.-C.,
RA Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;
RT "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
RT antibody W2 specifically reacts with condensed nuclei of
RT differentiated superficial cells.";
RL J. Cell Sci. 104:237-247(1993).
RN [2]
RP SEQUENCE OF 4-56.
RC TISSUE=Neutrophils;
RX MEDLINE=92304974; PubMed=1610833;
RA Dianoux A.-C., Stasia M.-J., Garin J., Gagnon J., Vignais P.V.;
RT "The 23-kilodalton protein, a substrate of protein kinase C, in bovine
RT neutrophil cytosol is a member of the S100 family.";
RL Biochemistry 31:5898-5905(1992).
CC -1- SUBUNIT: Disulfide linked heterodimer of a 7/11 kDa and a 22/23
CC kDa subunits.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; loosely associated to the
CC cytoskeleton.
CC -1- TISSUE SPECIFICITY: Found essentially in phagocytic cells.
CC -1- PTM: Phosphorylated by protein kinase C.
CC -1- SIMILARITY: Belongs to the S-100 family.
CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
DR HSSP; P06702; 1IRJ.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; PARTIAL.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Direct protein sequencing; Phosphorylation.
FT NON_TER 1
```

```
FT CA_BIND 19 32 EF-hand 1; low affinity (Potential).
FT CA_BIND 63 74 EF-hand 2; high affinity (Potential).
SQ SEQUENCE 122 AA; 13673 MW; F3CA8C48806BECCD CRC64;

Alignment Scores:
Pred. No.: 5.63 Length: 122
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S109_BOVIN (1-122)
QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
| | | | | | | | | | | | | | | | | | | | | |
Db 13 AsnilePheHisGlnTyrSerValArg 21

RESULT 8
Q6XE66
ID Q6XE66 PRELIMINARY; PRT; 402 AA.
AC Q6XE66;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Uvs121.
GN Name=uvs121;
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22894188; PubMed=14532085;
RX DOI=10.1128/AEM.69.10.6235-6242.2003;
RA Voget S., Leggewie C., Uesbeck A., Raasch C., Jaeger K.E.,
RA Streit W.R.;
RT "Prospecting for novel biocatalysts in a soil metagenome.";
RL Appl. Environ. Microbiol. 69:6235-6242(2003).
DR EMBL; AY236224; AAP70372.1; -.
DR InterPro; IPR010979; Ribosomal_H2TH.
DR InterPro; IPR001233; UPF0027.
DR Pfam; PF01139; UPF0027; 1.
SQ SEQUENCE 402 AA; 44013 MW; BDA6C97A81F8A509 CRC64;

Alignment Scores:
Pred. No.: 4.66 Length: 402
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x Q6XE66 (1-402)
QY 145 AAAGATAAAGCTGTCTATTGATGAATA 171
| | | | | | | | | | | | | | | | | | | | | |
Db 362 LysAspLysAlaValIleAspGluIle 370

RESULT 9
S106_HORSE
ID S106_HORSE STANDARD; PRT; 92 AA.
AC O77691;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcyclin.
GN Name=S100A6; Synonyms=CACY;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
```


DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF Hand like.
DR InterPro; IPR008080; Parvalbumin.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR01697; PARVALBUMIN.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 34 45 EF-hand 1 (Potential).
FT CA_BIND 66 77 EF-hand 2 (Potential).
FT CA_BIND 103 114 EF-hand 3 (Potential).
FT CA_BIND 144 155 EF-hand 4 (Potential).
SQ SEQUENCE 175 AA; 19743 MW; 583C5422ECD8B3C3 CRC64;

Alignment Scores:
Pred. No.: 56.8 Length: 175
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x CALB_ASHGO (1-175)

QY 205 GTGGACTTTTCAAGAAATTCATATCC 228
Db 73 ValAspPheGlnGluPheIleSer 80

RESULT 12
Q9H4U1
ID Q9H4U1 PRELIMINARY; PRT; 213 AA.
AC Q9H4U1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DJL4N1.2 (Novel S-100/ICaBP type calcium binding domain protein, similar to ttrichohyalin) (Fragment).
GN Name=dJL4N1.2;
OS Homo sapiens; (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; AL356504; CAC13173.1; -.
DR HSSP; P25815; 1J55.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
FT NON_TER 213 213
SQ SEQUENCE 213 AA; 24340 MW; B8C6E0810098E7D2 CRC64;

Alignment Scores:
Pred. No.: 55.1 Length: 213
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x Q9H4U1 (1-213)

QY 79 ACCCTCTTAAGGTGAGCTGAAG 102
Db 27 ThrLeuSerLysGlyGluLeuLys 34

RESULT 13
Q87I93
ID Q87I93 PRELIMINARY; PRT; 248 AA.
AC Q87I93;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VPA0713.
GN OrderedLocusNames=VPA0713;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RA "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005086; BAC62056.1; -.
DR InterPro; IPR001633; EAL.
DR Pfam; PF00563; EAL; 1.
DR SMART; SM00052; DUF2; 1.
DR PROSITE; PS50883; EAL; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 248 AA; 28942 MW; D9BB9097E2E84B6F CRC64;

Alignment Scores:
Pred. No.: 53.7 Length: 248
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x Q87I93 (1-248)

QY 189 AGCATCCAGGCTTGGAAATATTC 166
Db 181 SerIleGlnAlaLeuGluTyrPhe 188

RESULT 14
GLTF_ECOLI
ID GLTF_ECOLI STANDARD; PRT; 254 AA.
AC P28721;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Protein gltF precursor.
GN Name=gltF; OrderedLocusNames=b3214;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=93078627; PubMed=1447980;
RA Castano I., Flores N., Valle F., Covarrubias A.A., Bolivar F.;
RT "gltF, a member of the gltBDF operon of Escherichia coli, is involved in nitrogen-regulated gene expression.";
RL Mol. Microbiol. 6:2733-2741(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- FUNCTION: Involved in induction of the so-called NTR enzymes in
CC response to nitrogen deprivation, as well as in glutamate
CC biosynthesis. May mediate the glutamate-dependent repression of
CC the GLT operon.
CC -!- SIMILARITY: To E.coli yhcF.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; M74162; AAA23909.1; -.
DR EMBL; U18997; AAA58016.1; -.
DR EMBL; U00096; AAC76246.1; -.
DR PIR; S25281; S25281.
DR EchoBASE; EB1476; -.
DR EcoGene; EGI1514; gltF.
DR InterPro; IPR010546; DUF1120.
DR Pfam; PF06591; DUF1120; 1.
KW Complete proteome; Signal; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 254 Protein gltF.
FT TRANSMEM 213 229 Potential.
SQ SEQUENCE 254 AA; 26351 MW; 7424D7D1339A5F27 CRC64;

Alignment Scores:
Pred. No.: 53.5 Length: 254
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x GLTF_ECOLI (1-254)
Qy 254 GCAGCCTTCAGCGCAATGGCTACC 231
|||||
Db 19 AlaAlaPheSerAlaMetAlaThr 26

RESULT 15
Q72V46
ID Q72V46 PRELIMINARY; PRT; 264 AA.
AC Q72V46;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LIC10457;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
OS Copenhagen)
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiaceae; Leptospira.
OC NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fiocruz L1-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorry H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,

RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AE017288; AAS69078.1; -.
KW Complete proteome.
SQ SEQUENCE 264 AA; 30901 MW; A28C7BB1C128F79 CRC64;

Alignment Scores:
Pred. No.: 53.2 Length: 264
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x Q72V46 (1-264)
Qy 184 CCAGGCCTTGGAAATATTTTCATCAA 161
|||||
Db 139 ProGlyLeuGlyIlePheHisGln 146

Search completed: February 23, 2005, 12:38:15
Job time : 133 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:14:04 ; Search time 114 Seconds
(without alignments)
1872.734 Million cell updates/sec

Title: US-09-910-208B-12
Perfect score: 92
Sequence: 1 atgacaaaacttgaagagca.....attaccacaccacaaagag 276

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4105692 seqs, 386760381 residues

Word size: 1
Total number of hits satisfying chosen parameters: 3967864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO spool_p/HADDAD-09-910208B/runat_23022005_102315_15790/app_query.fasta.1
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=oligo.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208B @CGN_1_1 224 @runat_23022005_102315_15790 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	92	AAW03564	Aaw03564 Calcium b
2	92	100.0	92	AAW24137	Aaw24137 Human che
3	92	100.0	92	AAB45542	Aab45542 Human S10
4	92	100.0	92	AAB31911	Aab31911 Amino aci
5	92	100.0	92	AAB31907	Aab31907 Amino aci
6	92	100.0	92	AAB31908	Aab31908 Amino aci
7	92	100.0	92	ADA93649	Ada93649 Human cal
8	92	100.0	92	ADN04192	Adn04192 Antipsori
9	92	100.0	92	ADO19540	Ado19540 Human PRO
10	92	100.0	92	ADR14333	Adr14333 Human NF-

11	92	100.0	92	ADP23921	Adp23921 PRO polyp
12	92	100.0	92	ADS74331	Ads74331 PRO polyp
13	91	98.9	91	AAB31909	Aab31909 Amino aci
14	74	80.4	95	ABG27582	Abg27582 Novel hum
15	46	50.0	46	ABB43183	Abb43183 Peptide #
16	46	50.0	46	AAM37021	Aam37021 Peptide #
17	46	50.0	46	ABB26281	Abb26281 Protein #
18	46	50.0	46	AAM76914	Aam76914 Human bon
19	46	50.0	46	AAM64093	Aam64093 Human bra
20	46	50.0	46	ABG58579	Abg58579 Human liv
21	46	50.0	46	ABG46027	Abg46027 Human pep
22	23.9	23.9	363	ABG27581	Abg27581 Novel hum
23	9	9.8	90	AAAY90765	Aay90765 Bovine CA
24	9	9.8	90	AAAY90764	Aay90764 Bovine co
25	9	9.8	91	AAW01826	Aaw01826 Component
26	9	9.8	91	AAW93819	Aaw93819 Angiotrop
27	9	9.8	92	AAW03563	Aaw03563 Calcium b
28	8	8.7	8	ADB61382	Adb61382 Rheumatoi
29	8	8.8	70	ABP34077	Abp34077 Human ORF
30	8	8.7	202	ABG22271	Abg22271 Novel hum
31	8	8.7	206	ABP51289	Abp51289 Human MDD
32	8	8.7	218	AAW25257	Aam25257 Human pro
33	8	8.7	396	AAW23327	Aaw23327 Meripilus
34	8	8.8	516	ABP26046	Abp26046 Streptoco
35	8	8.7	542	ADN99439	Adn99439 Novel hum
36	8	8.7	1780	ABB71483	Abb71483 Drosophil
37	7	7.7	52	AAU61087	Aau61087 Propionib
38	7	7.7	52	ABM57606	Abm57606 Propionib
39	7	7.6	59	AAG77603	Aag77603 Human col
40	7	7.6	62	ADA36111	Ada36111 Acinetoba
41	7	7.7	84	AAO05978	Aao05978 Human pol
42	7	7.6	85	ABP41678	Abp41678 Human ova
43	7	7.7	86	ADK35063	Adk35063 Novel hum
44	7	7.7	90	AAAY91420	Aay91420 Human sec
45	7	7.7	91	AAAY91115	Aam91115 Human imm
46	7	7.7	93	ABG17471	Abg17471 Novel hum
47	7	7.6	93	ABU52339	Abu52339 Human GPC
48	7	7.6	93	ADL24013	Adl24013 Human NOV
49	7	7.6	99	AAAM39964	Aam39964 Human pol
50	7	7.6	106	ABU05340	Abu05340 Human dia
51	7	7.7	108	AAAM93932	Aam93932 Human pol
52	7	7.7	108	ADL32073	Adl32073 Human pro
53	7	7.6	112	AAW05275	Aaw05275 N-termina
54	7	7.6	113	AAW05274	Aaw05274 N-termina
55	7	7.6	113	AAAB45500	Aab45500 Murine in
56	7	7.6	113	ABG94296	Abg94296 Mouse int
57	7	7.6	113	ABG80608	Abg80608 Mouse mat
58	7	7.6	113	ADK17209	Adk17209 Mouse int
59	7	7.6	114	ADL05480	Adl05480 M. catarr
60	7	7.6	115	AAW05273	Aaw05273 N-termina
61	7	7.6	115	AAW72948	Aaw72948 Truncated
62	7	7.6	116	AAAB45502	Aab45502 Modified
63	7	7.6	116	AAAB45526	Aab45526 Modified
64	7	7.7	117	ADF59399	Adf59399 Human pol
65	7	7.6	121	ABG94350	Abg94350 Mouse C-I
66	7	7.6	121	ABG80662	Abg80662 Mouse IL-
67	7	7.6	121	ADK17221	Adk17221 Mouse C-I
68	7	7.6	122	AAAB45524	Aab45524 Modified
69	7	7.6	122	AAAB45527	Aab45527 Modified
70	7	7.6	122	AAAB45503	Aab45503 Modified
71	7	7.6	122	AAAB45504	Aab45504 Modified
72	7	7.6	122	AAAB45507	Aab45507 Modified
73	7	7.6	124	AAAB45523	Aab45523 Modified
74	7	7.6	124	AAAB45505	Aab45505 Modified
75	7	7.6	124	AAAB45501	Aab45501 Modified
76	7	7.7	124	ABG02537	Abg02537 Novel hum
77	7	7.6	128	AAAB45529	Aab45529 Modified
78	7	7.6	128	AAAB45525	Aab45525 Modified
79	7	7.6	128	AAAB45508	Aab45508 Modified
80	7	7.6	130	AAAB45506	Aab45506 Modified
81	7	7.6	130	AAAB45509	Aab45509 Modified
82	7	7.6	130	AAAB45528	Aab45528 Modified
83	7	7.6	133	AAAP71064	Aap71064 Murine eo

84	7	7.6	133	1	AAP82969	Aap82969 B cell di	C 157	7	7.7	229	6	ABR99450	Abr99450 Human sec
85	7	7.6	133	1	AAP80280	Aap80280 Murine pl	C 158	7	7.7	229	6	ABR98840	Abr98840 Human sec
86	7	7.6	133	2	AAR96963	Aar96963 T cell re	C 159	7	7.7	229	6	ABO16363	Abol6363 Human sec
87	7	7.6	133	2	AAW72949	Aaw72949 T cell re	C 160	7	7.7	229	6	ABR92263	Abr92263 Human sec
88	7	7.6	133	2	AAW72947	Aaw72947 T cell re	C 161	7	7.7	229	6	ABO18904	Abol8904 Human sec
89	7	7.6	133	4	AAB72618	Aab72618 Murine in	C 162	7	7.7	229	6	ABR78325	Abr78325 Human sec
90	7	7.6	133	4	AAB78557	Abp78557 N. gonorr	C 163	7	7.7	229	6	ABU71975	Abu71975 Novel hum
91	7	7.6	133	5	ABG94349	Abg94349 Mouse C-I	C 164	7	7.7	229	6	ABU85061	Abu85061 Novel hum
92	7	7.6	134	5	ABG80661	Abg80661 Mouse IL-	C 165	7	7.7	229	6	ABO00200	Abol00200 Novel hum
93	7	7.6	134	7	ADK17220	Adk17220 Mouse C-I	C 166	7	7.7	229	6	ABO11532	Abol11532 Human sec
94	7	7.6	136	5	ABG94348	Abg94348 Mouse C-I	C 167	7	7.7	229	6	ABO02177	Abol02177 Human sec
95	7	7.6	136	5	ABG80660	Abg80660 Mouse IL-	C 168	7	7.7	229	6	ABU88751	Abu88751 Novel hum
96	7	7.6	136	7	ADK17219	Adk17219 Mouse C-I	C 169	7	7.7	229	6	ABU83446	Abu83446 Human sec
97	7	7.6	139	3	ADQ66687	Adq66687 Novel hum	C 170	7	7.7	229	6	ABO06247	Abol06247 Novel hum
98	7	7.6	143	8	ADQ66687	Adq66687 Novel hum	C 171	7	7.7	229	6	ABR59283	Abr59283 Human sec
99	7	7.6	145	3	AAB45530	Aab45530 Modified	C 172	7	7.7	229	6	ABO09345	Abol09345 Human sec
100	7	7.6	149	4	ABG07201	Abg07201 Novel hum	C 173	7	7.7	229	6	ABO19209	Abol19209 Novel hum
101	7	7.6	160	7	ADC97442	Adc97442 E. faeciu	C 174	7	7.7	229	6	ABO11227	Abol11227 Human sec
102	7	7.6	163	7	ADI82689	Adi82689 Murine tr	C 175	7	7.7	229	6	ABR66845	Abr66845 Human sec
103	7	7.6	166	6	ABU40056	Abu40056 Protein e	C 176	7	7.7	229	6	ABO16058	Abol6058 Human sec
104	7	7.6	167	6	ABU41587	Abu41587 Protein e	C 177	7	7.7	229	6	ABO13764	Abol13764 Human sec
105	7	7.6	169	4	AAM39453	Aam39453 Human pol	C 178	7	7.7	229	6	ABU17529	Abu17529 Human sec
106	7	7.7	171	7	ADH88563	Adh88563 Enterococ	C 179	7	7.7	229	6	ABU65667	Abu65667 Human sec
107	7	7.6	172	8	ADN46597	Adn46597 Thermococ	C 180	7	7.7	229	6	ABO07515	Abol07515 Human PRO
108	7	7.6	175	2	AAV00881	Aay00881 Calcineur	C 181	7	7.7	229	6	ABO03702	Abol03702 Human sec
109	7	7.6	175	8	ADS43790	Ads43790 Bacterial	C 182	7	7.7	229	6	ABR67150	Abr67150 Human sec
110	7	7.7	184	7	ADE93878	Ades93878 Ixodes sc	C 183	7	7.7	229	6	ABO15753	Abol15753 Human sec
111	7	7.7	188	7	ADD30218	Add30218 Plant yie	C 184	7	7.7	229	6	ABU56034	Abu56034 Human PRO
112	7	7.7	188	8	ADI44051	Adi44051 Plant tra	C 185	7	7.7	229	6	ABU72310	Abu72310 Human PRO
113	7	7.7	194	4	AAB87433	Aab87433 Human gen	C 186	7	7.7	229	6	ABU65362	Abu65362 Human PRO
114	7	7.7	195	7	ABO80098	Abo80098 Pseudomon	C 187	7	7.7	229	6	ABU95307	Abu95307 Novel hum
115	7	7.6	201	8	ADS44352	Ads44352 Bacterial	C 188	7	7.7	229	6	ABU71210	Abu71210 Human PRO
116	7	7.6	201	4	AAM41239	Aam41239 Human pol	C 189	7	7.7	229	6	ABO07820	Abol07820 Human PRO
117	7	7.6	210	6	ABP79921	Abp79921 N. gonorr	C 190	7	7.7	229	6	ABR70061	Abr70061 Human sec
118	7	7.6	210	6	ABP76887	Abp76887 N. gonorr	C 191	7	7.7	229	6	ABR69394	Abr69394 Human sec
119	7	7.6	217	4	ABG13942	Abg13942 Novel hum	C 192	7	7.7	229	6	ABO01535	Abol01535 Human PRO
120	7	7.7	222	3	AAG14451	Aag14451 Arabidops	C 193	7	7.7	229	6	ABU81337	Abu81337 Human PRO
121	7	7.7	229	3	AAV66703	Aay66703 Membrane-	C 194	7	7.7	229	6	ABR60134	Abr60134 Human sec
122	7	7.7	229	4	AAU29122	Aau29122 Human PRO	C 195	7	7.7	229	6	ABU90983	Abu90983 Human PRO
123	7	7.7	229	4	AAB87549	Aab87549 Human PRO	C 196	7	7.7	229	6	ABR67869	Abr67869 Human sec
124	7	7.7	229	4	AAB65226	Aab65226 Human PRO	C 197	7	7.7	229	6	ABR65257	Abr65257 Human sec
125	7	7.7	229	5	ABG95874	Abg95874 Human sec	C 198	7	7.7	229	6	ABR68479	Abr68479 Human sec
126	7	7.7	229	6	ABU58498	Abu58498 Human PRO	C 199	7	7.7	229	6	ABR71891	Abr71891 Human sec
127	7	7.7	229	6	ABU88046	Abu88046 Novel hum	C 200	7	7.7	229	6	ABU59266	Abu59266 Human sec
128	7	7.7	229	6	ABU84361	Abu84361 Human sec	C 201	7	7.7	229	6	ABU85371	Abu85371 Human PRO
129	7	7.7	229	6	ABR66235	Abr66235 Human sec	C 202	7	7.7	229	6	ABU89061	Abu89061 Human sec
130	7	7.7	229	6	ABR56625	Abr56625 Human sec	C 203	7	7.7	229	6	ABU83141	Abu83141 Human sec
131	7	7.7	229	6	ABR59565	Abu59565 Human sec	C 204	7	7.7	229	6	ABU94997	Abu94997 Novel hum
132	7	7.7	229	6	ABU58041	Abu58041 Human PRO	C 205	7	7.7	229	6	ABU90545	Abu90545 Novel hum
133	7	7.7	229	6	ABU59119	Abu59119 Novel hum	C 206	7	7.7	229	6	ABU84056	Abu84056 Human sec
134	7	7.7	229	6	ABU82631	Abu82631 Human sec	C 207	7	7.7	229	6	ABU93707	Abu93707 Novel hum
135	7	7.7	229	6	ABU82804	Abu82804 Human PRO	C 208	7	7.7	229	6	ABO25963	Abol25963 Human PRO
136	7	7.7	229	6	ABR89925	Abu89925 Novel hum	C 209	7	7.7	229	6	ABR64952	Abr64952 Human sec
137	7	7.7	229	6	ABR68174	Abr68174 Human sec	C 210	7	7.7	229	6	ABO27304	Abol27304 Human sec
138	7	7.7	229	6	ABU60550	Abu60550 Human sec	C 211	7	7.7	229	6	ABR68784	Abr68784 Human sec
139	7	7.7	229	6	ABU96227	Abu96227 Novel hum	C 212	7	7.7	229	6	ABO06600	Abol06600 Human sec
140	7	7.7	229	6	ABU92658	Abu92658 Human sec	C 213	7	7.7	229	6	ABR99145	Abr99145 Human PRO
141	7	7.7	229	6	ABO08735	Abol08735 Human sec	C 214	7	7.7	229	6	ABU57029	Abu57029 Human PRO
142	7	7.7	229	6	ABO02787	Abol02787 Human sec	C 215	7	7.7	229	6	ABU85981	Abu85981 Novel hum
143	7	7.7	229	6	ABR74941	Abr74941 Human sec	C 216	7	7.7	229	6	ABU82268	Abu82268 Novel hum
144	7	7.7	229	6	ABR94703	Abu94703 Human PRO	C 217	7	7.7	229	6	ABU87279	Abu87279 Human PRO
145	7	7.7	229	6	ABU13932	Abu13932 Human sec	C 218	7	7.7	229	6	ABU83751	Abu83751 Human sec
146	7	7.7	229	6	ABU85676	Abu85676 Human PRO	C 219	7	7.7	229	6	ABO08125	Abol08125 Human PRO
147	7	7.7	229	6	ABU98836	Abu98836 Novel hum	C 220	7	7.7	229	6	ABU92499	Abu92499 Human sec
148	7	7.7	229	6	ABU98051	Abu98051 Novel hum	C 221	7	7.7	229	6	ABU81836	Abu81836 Novel hum
149	7	7.7	229	6	ABU91757	Abu91757 Novel hum	C 222	7	7.7	229	6	ABU66000	Abu66000 Novel hum
150	7	7.7	229	6	ABU89450	Abu89450 Human PRO	C 223	7	7.7	229	6	ABU81169	Abu81169 Human sec
151	7	7.7	229	6	ABU86291	Abu86291 Human sec	C 224	7	7.7	229	6	ABR59829	Abr59829 Human sec
152	7	7.7	229	6	ABU67504	Abu67504 Human sec	C 225	7	7.7	229	6	ABU94017	Abu94017 Novel hum
153	7	7.7	229	6	ABU80532	Abu80532 Human PRO	C 226	7	7.7	229	6	ABU99870	Abu99870 Novel hum
154	7	7.7	229	6	ABU72517	Abu72517 Novel hum	C 227	7	7.7	229	6	ABR66540	Abr66540 Human sec
155	7	7.7	229	6	ABU90899	Abu90899 Novel hum	C 228	7	7.7	229	6	ABR90958	Abr90958 Human sec
156	7	7.7	229	6	ABO33958	Abol33958 Human sec	C 229	7	7.7	229	6	ABO53284	Abol53284 Novel hum

C 230	7	7.7	229	6	ABU58972	Human sec
C 231	7	7.7	229	6	ABU94385	Human PRO
C 232	7	7.7	229	6	ABU79267	Human PRO
C 233	7	7.7	229	6	ABU86596	Human sec
C 234	7	7.7	229	6	ABU86901	Novel hum
C 235	7	7.7	229	6	ABU94690	Human PRO
C 236	7	7.7	229	6	ABO04617	Human PRO
C 237	7	7.7	229	6	ABR70366	Human sec
C 238	7	7.7	229	6	ABU92350	Novel hum
C 239	7	7.7	229	6	ABU98531	Human PRO
C 240	7	7.7	229	6	ABR65930	Human sec
C 241	7	7.7	229	6	ABR64647	Human sec
C 242	7	7.7	229	6	ABU59415	Novel hum
C 243	7	7.7	229	6	ABU79572	Human PRO
C 244	7	7.7	229	6	ABU92963	Human sec
C 245	7	7.7	229	6	ABU95922	Human PRO
C 246	7	7.7	229	6	ABU91142	Novel hum
C 247	7	7.7	229	6	ABU90235	Novel hum
C 248	7	7.7	229	6	ABO09650	Human sec
C 249	7	7.7	229	6	ABO10922	Human sec
C 250	7	7.7	229	6	ABR70976	Human sec
C 251	7	7.7	229	6	ABU98286	Human sec
C 252	7	7.7	229	6	ABU87584	Human PRO
C 253	7	7.7	229	6	ABU91452	Human PRO
C 254	7	7.7	229	6	ABU89291	Novel hum
C 255	7	7.7	229	6	ABU84666	Human sec
C 256	7	7.7	229	6	ABR69756	Human sec
C 257	7	7.7	229	6	ABU80133	Human PRO
C 258	7	7.7	229	6	ABU82498	Human PRO
C 259	7	7.7	229	6	ABU92181	Novel hum
C 260	7	7.7	229	6	ABU93402	Human PRO
C 261	7	7.7	229	6	ABO09955	Human sec
C 262	7	7.7	229	6	ABO09040	Human sec
C 263	7	7.7	229	6	ABU96462	Human PRO
C 264	7	7.7	229	6	ABU10887	Human PRO
C 265	7	7.7	229	6	ABU10608	Human sec
C 266	7	7.7	229	6	ABU81639	Novel hum
C 267	7	7.7	229	6	ABU72132	Human PRO
C 268	7	7.7	229	6	ABU95617	Human PRO
C 269	7	7.7	229	6	ABU96826	Novel hum
C 270	7	7.7	229	6	ABR70671	Human sec
C 271	7	7.7	229	6	ABO05022	Novel hum
C 272	7	7.7	229	6	ABO08430	Human sec
C 273	7	7.7	229	6	ABU88578	Human sec
C 274	7	7.7	229	6	ABO34092	Human PRO
C 275	7	7.7	229	6	ABO05637	Human sec
C 276	7	7.7	229	6	ABR74026	Human sec
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C 286	7	7.7	229	6	ABO40465	Human sec
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C 289	7	7.7	229	6	ADA77950	Human sec
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C 294	7	7.7	229	6	ABR95008	Human sec
C 295	7	7.7	229	6	ABR95313	Human sec
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Abm29094	Human sec					
Abm07070	Human sec					
Abm21164	Human sec					
Abm09510	Human sec					
Abm41380	Human sec					
Abm36195	Human PRO					
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Abm36500	Human sec					
Abm35585	Human PRO					
Abm39550	Human sec					
Abm10425	Human sec					
Abm11950	Human sec					
Abm52096	Human PRO					
Abm52401	Human PRO					
Ada19910	Novel hum					
Abm23719	Human sec					
Abm17293	Human tra					
Ada17786	Human PRO					
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Abm86993	Human sec					
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Abm28179	Human sec					
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Abm06460	Human sec					
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Abm33180	Human sec					
Abm52706	Human PRO					
Abm50266	Human sec					
Abm99260	Human sec					
Abm04312	Human sec					
Abm05942	Human sec					
Abm18482	Human sec					
Ada27894	Human sec					
Abm97510	Human sec					

C 376	7	7.7	229	6	ABR80610	Human sec
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C 407	7	7.7	229	6	ABO22161	Human sec
C 408	7	7.7	229	6	ADA20082	Novel hum
C 409	7	7.7	229	6	ABO34190	Human sec
C 410	7	7.7	229	6	ABR96595	Human sec
C 411	7	7.7	229	6	ADA94474	Human sec
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C 419	7	7.7	229	6	ABO38330	Human sec
C 420	7	7.7	229	6	ABO45630	Human PRO
C 421	7	7.7	229	6	ABM20554	Human sec
C 422	7	7.7	229	6	ADA81469	Human sec
C 423	7	7.7	229	6	ABO16668	Human sec
C 424	7	7.7	229	6	ABO18294	Human sec
C 425	7	7.7	229	6	ABO22721	Human PRO
C 426	7	7.7	229	6	ABO23026	Human PRO
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C 434	7	7.7	229	6	ABO30348	Human sec
C 435	7	7.7	229	6	ABM07375	Human sec
C 436	7	7.7	229	6	ABM03966	Human sec
C 437	7	7.7	229	6	ABO37110	Human sec
C 438	7	7.7	229	6	ABO41685	Human sec
C 439	7	7.7	229	6	ABO35280	Human PRO
C 440	7	7.7	229	6	ABM25129	Human sec
C 441	7	7.7	229	6	ABO47521	Human sec
C 442	7	7.7	229	6	ABO47826	Human sec
C 443	7	7.7	229	6	ABO48436	Human sec
C 444	7	7.7	229	6	ABO51486	Human PRO
C 445	7	7.7	229	6	ABO51791	Human PRO
C 446	7	7.7	229	6	ABO50571	Human sec
C 447	7	7.7	229	6	ABR79695	Human sec
C 448	7	7.7	229	6	ABR79695	Human sec
C 449	7	7.7	229	6	ABM16957	Human sec
C 450	7	7.7	229	6	ABO17989	Human sec
C 451	7	7.7	229	6	ABO20941	Human sec
C 452	7	7.7	229	6	ABR96900	Human sec
C 453	7	7.7	229	6	ADA38699	Human sec
C 454	7	7.7	229	6	ABM12255	Human sec
C 455	7	7.7	229	6	ABM16347	Human sec
C 456	7	7.7	229	6	ABM24214	Human sec
C 457	7	7.7	229	6	ABM14695	Human sec
C 458	7	7.7	229	6	ABM04576	Human sec
C 459	7	7.7	229	6	ABM06765	Human sec
C 460	7	7.7	229	6	ABM09205	Human sec
C 461	7	7.7	229	6	ABO39245	Human sec
C 462	7	7.7	229	6	ABM75510	Human sec
C 463	7	7.7	229	6	ABM25434	Human sec
C 464	7	7.7	229	6	ABM19944	Human sec
C 465	7	7.7	229	6	ABO46850	Human PRO
C 466	7	7.7	229	6	ABO47155	Human PRO
C 467	7	7.7	229	6	ADA83267	Human sec
C 468	7	7.7	229	6	ABR71586	Human sec
C 469	7	7.7	229	6	ABR72196	Human sec
C 470	7	7.7	229	6	ABR98535	Human sec
C 471	7	7.7	229	6	ABO06905	Human sec
C 472	7	7.7	229	6	ABR84858	Human sec
C 473	7	7.7	229	6	ABR73416	Human sec
C 474	7	7.7	229	6	ABR76510	Human sec
C 475	7	7.7	229	6	ABR73111	Human sec
C 476	7	7.7	229	6	ABM18177	Human sec
C 477	7	7.7	229	6	ABO20636	Human sec
C 478	7	7.7	229	6	ABO25379	Human PRO
C 479	7	7.7	229	6	ABO25684	Human PRO
C 480	7	7.7	229	6	ABR94093	Human sec
C 481	7	7.7	229	6	ADA92820	Human sec
C 482	7	7.7	229	6	ABR80000	Human sec
C 483	7	7.7	229	6	ABM11340	Human sec
C 484	7	7.7	229	6	ABO32947	Human PRO
C 485	7	7.7	229	6	ABO30653	Human sec
C 486	7	7.7	229	6	ABO30958	Human sec
C 487	7	7.7	229	6	ABM27264	Human sec
C 488	7	7.7	229	6	ABM30009	Human sec
C 489	7	7.7	229	6	ABM05545	Human sec
C 490	7	7.7	229	6	ABM15610	Human sec
C 491	7	7.7	229	6	ABM08595	Human sec
C 492	7	7.7	229	6	ABO42295	Human sec
C 493	7	7.7	229	6	ABO38025	Human PRO
C 494	7	7.7	229	6	ABO45935	Human sec
C 495	7	7.7	229	6	ABM66738	Human sec
C 496	7	7.7	229	6	ADB20310	Human sec
C 497	7	7.7	229	6	ABM19639	Human sec
C 498	7	7.7	229	6	ABO49351	Human sec
C 499	7	7.7	229	6	ABO49656	Human sec
C 500	7	7.7	229	8	ADH98930	Novel hum

ALIGNMENTS

RESULT 1

AAW03564

ID AAW03564 standard; protein; 92 AA.

XX

XX AAW03564;

XX

DT 01-MAY-1997 (first entry)

XX

DE Calcium binding protein CAAF1.

XX

KW Calcium binding protein; human; amniotic fluid; s100 protein family;

KW intracellular signal transduction; squamous epithelial cell; neutrophil;

KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;

KW squamous cell carcinoma; skin; oesophagus; CAAF1; lung; blood disease.

XX

OS Homo sapiens.

XX

PN EP731166-A2:
XX
PD 11-SEP-1996:
XX
PF 04-DEC-1995; 95EP-00119045.
XX
PR 06-MAR-1995; 95JP-00045564.
PR 06-MAR-1995; 95JP-00070468.
XX
PA (TOFU) TONEN CORP.
PA (HITO/) HITOMI J.
XX
PI Hitomi J, Yamaguchi K, Yamamura T, Kimura T;
XX
XX WPI; 1996-403989/41.
DR N-PSDB; AAT39346.
XX
PT New human or bovine calcium binding protein and related nucleic acid - is
PT a marker for inflammation, neoplasia, skin and blood diseases.
XX
PS Claim 1; Page 24; 36pp; English.
XX
CC This sequence represents the CAAF1 calcium-binding protein isolated from
CC human amniotic fluid. CAAF1 belongs to the S100 protein family, which
CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion
CC concentration is one of the key factors for intracellular signal
CC transduction. The calcium signals are transduced by various calcium-
CC binding proteins, such as this protein. CAAF1 is normally expressed in
CC squamous epithelial cells, neutrophils and macrophages, but atypical
CC epithelial cells are negative for CAAF1 and overexpression is observed in
CC several types of cancer cells and neutrophils/macrophages infiltrating
CC cancerous lesions. Detection of CAAF1 (using antibodies in usual
CC immunoassays) can be used to diagnose (or monitor) inflammation,
CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,
CC lung and cervix), and skin and blood diseases
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x AAW03564 (1-92)

Qy 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
Qy 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
Qy 121 CTGTCAAACACCATCAAGAATATCAAAGATAAAGCTGTCAATTGATGAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
Qy 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
Qy 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 2
AAW24137
ID AAW24137 standard; protein; 92 AA.
XX
AC AAW24137;

XX 28-JAN-1998 (first entry)
DT
XX Human chemotactic cytokine I.
DE
XX chemotactic cytokine; tumour; autoimmune disease; antagonist; agonist.
KW
XX Homo sapiens.
OS
XX WO9723640-A1.
PN
XX 03-JUL-1997.
PD
XX
PF 26-DEC-1995; 95WO-US016871.
XX
PR 26-DEC-1995; 95WO-US016871.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Alfonso P, Gentz R, Su JY;
XX
XX WPI; 1997-351075/32.
DR N-PSDB; AAT85774.
DR
XX DNA encoding chemotactic cytokine I - used to treat, e.g. tumours,
PT chronic infection, leukaemia, etc.
XX
PS Claim 12; Page 48-49; 64pp; English.
XX
CC This is a human chemotactic cytokine I polypeptide. The encoding
CC polynucleotide, along with a vector and a host cell can be used for the
CC recombinant production of the chemotactic cytokine. Cytokine agonists and
CC antagonists can be used for the treatment of a patient requiring a
CC chemotactic cytokine I and for the treatment of a patient requiring the
CC inhibition of a chemotactic cytokine I polypeptide, respectively. The
CC chemotactic cytokine is used to treat tumours, chronic infection,
CC leukaemia and T-cell mediated autoimmune diseases
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x AAW24137 (1-92)

Qy 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
Qy 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
Qy 121 CTGTCAAACACCATCAAGAATATCAAAGATAAAGCTGTCAATTGATGAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
Qy 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
Qy 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3
AAB45542
ID AAB45542 standard; protein; 92 AA.

Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31911 (1-92)

QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCGAAACACCATCAAGAATATCAAGATAAAGCTGTCTCATTTGATGAAATATTCGAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 5

AAB31907

ID AAB31907 standard; protein; 92 AA.

XX AC AAB31907;

XX 15-MAY-2001 (first entry)

XX DE Amino acid sequence of a human protein.

XX KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine; ganglioside GM2 activator; saposin B; degenerative disease; glial cell; neurological disease; auto-immune disease; multiple sclerosis; toxicity; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; rheumatoid polyarthriti; lupus erythematosus; gene therapy.

XX OS Homo sapiens.

XX PN WO200105422-A2.

XX PD 25-JAN-2001.

XX PF 17-JUL-2000; 2000WO-FR002057.

XX PR 15-JUL-1999; 99FR-00009372.

XX PA (INMR) BIOMERIEUX STELHYS.

XX PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;

XX DR WPI; 2001-159475/16.

XX PT Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.

XX PS Claim 1; Page 166-167; 209pp; French.

XX CC The present sequence represents a human protein, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polynucleotide sequence belonging to the perlecan, precursor of the retinol-binding plasma protein, precursor of the ganglioside GM2 activator, calgranulin B or saposin B protein families. The method is used for detecting, preventing or treating a degenerative, neurological and/or auto-immune disease. The

CC polynucleotides and polypeptides are used for diagnosis, prognosis, prevention and treatment of multiple sclerosis (in its various forms and phases). They may also be useful in cases of e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid polyarthriti and lupus erythematosus, including use as vaccines and in gene therapy (expression of sense or antisense sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells

XX SQ Sequence 92 AA;

Alignment Scores:

Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31907 (1-92)

QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCGAAACACCATCAAGAATATCAAGATAAAGCTGTCTCATTTGATGAAATATTCGAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 6

AAB31908

ID AAB31908 standard; protein; 92 AA.

XX AC AAB31908;

XX DT 15-MAY-2001 (first entry)

XX DE Amino acid sequence of a human protein.

XX KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine; ganglioside GM2 activator; saposin B; degenerative disease; glial cell; neurological disease; auto-immune disease; multiple sclerosis; toxicity; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; rheumatoid polyarthriti; lupus erythematosus; gene therapy.

XX OS Homo sapiens.

XX PN WO200105422-A2.

XX PD 25-JAN-2001.

XX PF 17-JUL-2000; 2000WO-FR002057.

XX PR 15-JUL-1999; 99FR-00009372.

XX PA (INMR) BIOMERIEUX STELHYS.

XX PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;

XX DR WPI; 2001-159475/16.

PT Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand.
XX
PS Claim 1; Page 167; 209pp; French.
XX
CC The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4
US-09-910-208B-12 (1-276) x AAB31908 (1-92)
QY 1 ATGACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAACACCATCAAGAATATCAAGATATAAGCTGTTCATTGATGAATATTCGAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGTGCCCATACACACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 7
ADA93649
ID ADA93649 standard; protein; 92 AA.
XX
AC ADA93649;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human calgranulin C protein SEQ ID NO:2.
XX
KW inflammatory disease; calgranulin C; antiinflammatory; gene therapy;
KW vasculitis; Kawasaki disease; cystic fibrosis;
KW chronic inflammatory disease; ulcerative colitis; Crohn's disease;
KW chronic bronchitis; inflammatory arthritis; psoriatic arthritis;
KW rheumatoid arthritis; seronegative arthritis;
KW systemic onset juvenile rheumatoid arthritis; SORA; Still's disease;
KW acute inflammation; human.
XX
OS Homo sapiens.

XX WO2003069341-A2.
PN
XX 21-AUG-2003.
PD
XX 17-FEB-2003; 2003WO-EP001575.
PF
XX 15-FEB-2002; 2002US-00077600.
PR
XX (SWIT-) SWITCH BIOTECH AG.
PA (SORG/) SORG C.
PA (ROTH/) ROTH J.
XX Sorg C, Roth J;
PI WPI; 2003-671681/63.
XX N-PSDB; ADA93648.
DR
XX Diagnosing, treating or preventing inflammatory diseases comprises
PT determining the amount and/or concentration of CALGRANULIN C polypeptide
PT and/or nucleic acids encoding the polypeptide present in a biological
PT sample.
XX
PS Claim 7; Page 64; 64pp; English.

XX The present invention describes a method for diagnosing inflammatory
CC diseases, which comprises determining the amount and/or concentration of
CC calgranulin C polypeptide and/or nucleic acids encoding the polypeptide
CC present in the biological sample. Also described are methods for treating
CC or preventing an inflammatory disease in a mammal, and medical treatment
CC of the mammal, where the treatment is based on the stage of the disease
CC to be treated or prevented. Calgranulin C has antiinflammatory activity
CC and can be used in gene therapy. The method is useful for diagnosing,
CC treating or preventing inflammatory diseases, e.g. vasculitis
CC (particularly Kawasaki disease), cystic fibrosis, chronic inflammatory
CC diseases like ulcerative colitis or Crohn's disease, chronic bronchitis, or
CC inflammatory arthritis (e.g. psoriatic arthritis, rheumatoid arthritis or
CC seronegative arthritis), systemic onset juvenile rheumatoid arthritis
CC (SORA or Still's disease), acute inflammation above the background of a
CC chronic inflammation, an acquired infection on the background of an
CC inflammatory disease, or an exacerbation of an already present disease.
CC The method is also useful for diagnosing specific stages of inflammatory
CC diseases, for determining the risk of relapse, and for discriminating
CC between diseases with similar symptoms. The present sequence represents
CC human calgranulin C, which is used in the exemplification of the present
CC invention.

XX Sequence 92 AA;
SQ
Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7

US-09-910-208B-12 (1-276) x ADA93649 (1-92)
QY 1 ATGACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAACACCATCAAGAATATCAAGATATAAGCTGTTCATTGATGAATATTCGAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGGTAGCCATT 240

Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGGCTGCCATTACACACCCACAAAGAG 276

Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 8

ADN04192

ID ADN04192 standard; protein; 92 AA.

XX

AC ADN04192;

XX

DT 01-JUL-2004 (first entry)

XX

DE Antipsoriatic protein sequence #291.

XX

KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX

OS Homo sapiens.

XX

PN WO2004028479-A2.

XX

PD 08-APR-2004.

XX

PF 25-SEP-2003; 2003WO-US030907.

XX

PR 25-SEP-2002; 2002US-0414006P.

XX

PA (GETH) GENENTECH INC.

XX

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

PI Wu TD;

XX

DR WPI; 2004-305105/28.

DR N-PSDB; ADN04191.

XX

PT New PRO nucleic acid or polypeptide, useful for preparing a

PT pharmaceutical composition for diagnosing or treating psoriasis in a

PT mammal.

XX

PS Claim 9; SEQ ID NO 586; 3069pp; English.

XX

CC The invention relates to novel polynucleotide and polypeptides for

CC treating psoriasis or a sequence having at least 80% identity to the

CC above sequences. The nucleic acid is useful for preparing a composition

CC for diagnosing or treating psoriasis in a mammal. This sequence

CC corresponds to one of the polypeptides of the invention.

XX

SQ Sequence 92 AA;

Alignment Scores:

Pred. No.: 1.04e-80 Length: 92

Score: 92.00 Matches: 92

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADN04192 (1-92)

QY 1 ATGACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60

Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCTCTCTAAGGGTGAGCTGAAGCAGCTGTACAAAGGAG 120

Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCGAACACCATCAAGAATATCAAGATAAAGCTGTTCATTGATGAATATTTCCAAGGC 180

Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTATATCCCTGGTAGCCATT 240

Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGGCTGCCATTACACACCCACAAAGAG 276

Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 9

ADO19540

ID ADO19540 standard; protein; 92 AA.

XX

AC ADO19540;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human PRO polypeptide #235.

XX

KW Human; PRO; immune related disorder; systemic lupus erythematosus;

KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;

KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;

KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;

KW diabetes mellitus; renal disease; demyelinating disease;

KW central nervous system; peripheral nervous system;

KW demyelinating polyneuropathy; Guillain-Barre syndrome;

KW chronic inflammatory demyelinating polyneuropathy.

XX

OS Homo sapiens.

XX

PN WO2004043361-A2.

XX

PD 27-MAY-2004.

XX

PF 06-NOV-2003; 2003WO-US035268.

XX

PR 08-NOV-2002; 2002US-0425235P.

XX

PA (GETH) GENENTECH INC.

XX

PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;

PI Wood WI, Wu TD;

XX

DR WPI; 2004-420067/39.

DR N-PSDB; ADO19539.

XX

PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for

PT treating an immune related disorder such as systemic lupus erythematosus,

PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or

PT spondyloarthropathy.

XX

PS Claim 7; SEQ ID NO 470; 1731pp; English.

XX

CC The invention relates to human PRO polypeptides and the polynucleotides

CC encoding them. The polypeptides and polynucleotides are useful for

CC treating and diagnosing immune related disorders in mammals. The immune

CC related disorders include systemic lupus erythematosus, rheumatoid

CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic

CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune

CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes

CC mellitus, immune-mediated renal disease, demyelinating diseases of the

CC central or peripheral nervous system, demyelinating polyneuropathy,

CC Guillain-Barre syndrome and chronic inflammatory demyelinating

CC polyneuropathy. This sequence represents a human PRO polypeptide of the

CC invention.

XX

SQ Sequence 92 AA;

Alignment Scores:

Pred. No.: 1.04e-80 Length: 92

Score: 92.00 Matches: 92

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

PS Claim 6; SEQ ID NO 334; 237pp; English.

XX This invention relates to the novel association of protein sequences (and

CC the genes which encode them) to the NF-kappaB pathway. The invention may

CC be useful for the production of compounds with an antiinflammatory,

CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,

CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,

CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or

CC vulnery activity or for gene therapy. The proteins and nucleotides are

CC useful for diagnosing, preventing, treating, or ameliorating conditions

CC or diseases associated with the NF-kappaB pathway. The condition is an

CC immune disorder, an inflammatory disorder, an inflammatory disorder

CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,

CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM

CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic

CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,

CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell

CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory

CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick

CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper

CC immune activity, disorders related to aberrant acute phase responses,

CC hypercongenital conditions, birth defects, necrotic lesions, wounds,

CC organ transplant rejection, conditions related to organ transplant

CC rejection, disorders related to aberrant signal transduction,

CC proliferating disorders, cancers and HIV propagation in cells infected

CC with other viruses. The present sequence is that of a human protein which

CC is subject to the novel association with the NF-kappaB pathway of the

CC invention. Note: This sequence does not appear in the specification but

CC was obtained by the indexer from Genbank.

XX

SQ Sequence 92 AA;

Alignment Scores:

Pred. No.:	1.04e-80	Length:	92
Score:	92.00	Matches:	92
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-09-910-208B-12 (1-276) x ADR14333 (1-92)

QY	1	ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT	60
Db	1	MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal	20
QY	61	CGGAAGGGGCAATTTGACACCCCTCTTAAGGGTGAGTGAAGCAGCTGCTTACAAGGAG	120
Db	21	ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu	40
QY	121	CTTGCAAAACACCATCAAGAATATCAAGATAAAGCTGTGATGATGAATATTTCCAAGGC	180
Db	41	LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly	60
QY	181	CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAAATTCATATCCCTGGTAGCCATT	240
Db	61	LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle	80
QY	241	GGCTGAAGGCTGCCCATTTACCACACCCCAAAAGAG	276
Db	81	AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu	92

RESULT 11

ADP23921

ID ADP23921 standard; protein; 92 AA.

XX

AC ADP23921;

XX

DT 18-NOV-2004 (first entry)

XX

DE PRO polypeptide SEQ ID NO:1099.

XX

KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

US-09-910-208B-12 (1-276) x ADO19540 (1-92)

QY	1	ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT	60
Db	1	MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal	20
QY	61	CGGAAGGGGCAATTTGACACCCCTCTTAAGGGTGAGTGAAGCAGCTGCTTACAAGGAG	120
Db	21	ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu	40
QY	121	CTTGCAAAACACCATCAAGAATATCAAGATAAAGCTGTGATGATGAATATTTCCAAGGC	180
Db	41	LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly	60
QY	181	CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAAATTCATATCCCTGGTAGCCATT	240
Db	61	LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle	80
QY	241	GGCTGAAGGCTGCCCATTTACCACACCCCAAAAGAG	276
Db	81	AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu	92

RESULT 10

ADR14333

ID ADR14333 standard; protein; 92 AA.

XX

AC ADR14333;

XX

DT 21-OCT-2004 (first entry)

XX

DE Human NF-kappaB pathway-associated protein SeqID334.

XX

KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;

KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;

KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;

KW immunosuppressive; vulnery; gene therapy; immune disorder;

KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;

KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;

KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;

KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;

KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;

KW viral replication; host cell survival; evasion of immune response;

KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;

KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;

KW autoimmune disorder; hyper immune activity;

KW aberrant acute phase response; hypercongenital condition; birth defect;

KW necrotic lesion; wound; organ transplant rejection;

KW aberrant signal transduction; proliferating disorder; cancer;

KW HIV propagation; human.

XX

OS Homo sapiens.

XX

PN WO2004065577-A2.

XX

PD 05-AUG-2004.

XX

PF 13-JAN-2004; 2004WO-US000798.

XX

PR 14-JAN-2003; 2003US-0440068P.

PR

PR 12-MAY-2003; 2003US-0469757P.

XX

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Nadler SG, Neubauer MG, Feder JN, Carman J;

XX

XX WPI; 2004-562168/54.

DR

DR N-PSDB; ADR14332.

XX

XX New isolated polynucleotides and polypeptides associated with NF-kappaB

PT pathway, useful for diagnosing, treating, or preventing disorders or

PT diseases associated with NF-kappaB pathway.

XX

KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS Unidentified.
XX WO2004041170-A2.
PN
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-419628/39.
DR N-PSDB; ADP23920.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 7; SEQ ID NO 1099; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADP23921 (1-92)

QY 1 ATGACAAACTTGAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
|||||
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120

Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
|||||
QY 121 CTTGCAAAACACCATCAAGAATATCAAAAGATAAAGCTGTGTCATTGATGAATATTCGAAGGC 180
|||||
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
|||||
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATT 240
|||||
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
|||||
QY 241 GCGCTGAAGGCTGCCCATTAACACACCCACAAAGAG 276
|||||
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
|||||
RESULT 12
ADS74331
ID ADS74331 standard; protein; 92 AA.
XX
AC ADS74331;
XX
DT 16-DEC-2004 (first entry)
XX
DE PRO polypeptide PRO62943, role in immune-related disease.
XX
KW PRO62943; rheumatoid arthritis; psoriasis; antirheumatic; antiarthritic;
KW antipsoriatic; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 4..47
FT /note= "S-100/ICaBP type calcium binding domain"
FT Region 60..65
FT /note= "N-myristoylation site"
XX
PN WO2004081199-A2.
XX
PD 23-SEP-2004.
XX
PF 10-MAR-2004; 2004WO-US007862.
XX
PR 11-MAR-2003; 2003US-0454025P.
XX (GETH) GENENTECH INC.
PI Baldwin D, Bodary S, Clark H, Fong S, Gurney AL, Williams PM;
XX
DR WPI; 2004-668955/65.
DR N-PSDB; ADS74330.
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating psoriasis, Crohn's disease, Ulcerative Colitis, or rheumatoid
PT arthritis.
XX
PS Claim 9; SEQ ID NO 50; 166pp; English.
XX
CC The present sequence is the protein sequence of novel human PRO
CC polypeptide PRO62943. The invention provides newly identified and
CC isolated nucleotide sequences encoding polypeptides referred to as PRO
CC polypeptides that are useful in the diagnosis and treatment of immune-
CC related diseases. Microarray analysis showed that expression of PRO62943
CC is up-regulated 4-fold in lesional skin as compared to non-lesional skin
CC from psoriasis patients and up-regulated 2-fold in white blood cells from
CC rheumatoid arthritis patients as compared to those from healthy donors.
CC It is also down-regulated 2-fold upon activation of CD4 T cells with CD28
CC or ICAM, down-regulated 6-fold upon differentiation of monocytes into
CC macrophages after 7 days in differentiation media and up-regulated 4-fold
CC upon activation of monocytes with LPS. PRO62943 can be used in a claimed
CC method of identifying a compound that inhibits expression of the gene
CC encoding it. The candidate compound is especially an antisense nucleic
CC acid. The PRO polypeptide can be obtained by recombinant expression,
CC especially in CHO, Escherichia coli or yeast host cells. The polypeptide,

CC its antagonist or an antibody that binds the polypeptide are used in
CC claimed methods for the alleviation or diagnosis of rheumatoid arthritis
CC and psoriasis.

XX SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADS74331 (1-92)

Qy 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
Qy 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGTGAGCTGAAGCAGCTGCTTACAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
Qy 121 CTTGCAAAACACCATCAAGAATATCAAAGATAAAGCTGTCTATGATGAAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
Qy 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
Qy 241 GCGTGAAGGCTGCCCATTTACCACACCCCAAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 13
AAB31909
ID AAB31909 standard; protein; 91 AA.
XX
AC AAB31909;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a human protein.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.

XX
OS Homo sapiens.
XX
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-FR002057.
XX
PR 15-JUL-1999; 99FR-00009372.
XX
PA (INMR) BIOMERIEUX STELHYS.
XX
PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX
DR WPI; 2001-159475/16.
XX
PT Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand.
XX
PS Claim 1; Page 167; 209pp; French.

XX The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells

XX SQ Sequence 91 AA;

Alignment Scores:
Pred. No.: 9.86e-80 Length: 91
Score: 91.00 Matches: 91
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.91% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31909 (1-91)

Qy 4 ACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTTCCG 63
Db 1 ThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerValArg 20
Qy 64 AAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAGGAGCTT 123
Db 21 LysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGluLeu 40
Qy 124 GCAAACACCATCAAGAATATCAAGATAAAGCTGTCTAATTGATGAATATTTCCAAGGCCTG 183
Db 41 AlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60
Qy 184 GATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80
Qy 244 CTGAAGGCTGCCCATTTACCACACCCCAAAAGAG 276
Db 81 LeuLysAlaAlaHisTyrHisThrHisLysGlu 91

RESULT 14
ABG27582
ID ABG27582 standard; protein; 95 AA.
XX
AC ABG27582;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27573.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR N-PSDB; AAS91769.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 57941; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 95 AA;
Alignment Scores:
Pred. No.: 3.67e-63 Length: 95
Score: 74.00 Matches: 74
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 80.43% Indels: 0
DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x ABG27582 (1-95)
QY 55 TCAGTTCGGAAGGGCATTCTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACA 114
Db 22 SerValArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThr 41
QY 115 AAGGAGCTTGCAACACCATCAAGAATATCAAGATAAAGCTGTCATTGATGAATATTC 174
Db 42 LysGluLeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePhe 61
QY 175 CAAGGCTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAAATTCATATCCCTGGTA 234
Db 62 GlnGlyLeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuVal 81
QY 235 GCCATTGCGCTGAAGGCTGCCATTACCACACCCACAAAGAG 276
Db 82 AlaIleAlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 95
RESULT 15
ABB43183
ID ABB43183 standard; peptide; 46 AA.
XX
AC ABB43183;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #10689: encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.
KW Homo sapiens.
XX
XX WO200157277-A2.
PN
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483447/52.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 35818; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 46 AA;
Alignment Scores:
Pred. No.: 8.14e-36 Length: 46
Score: 46.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x ABB43183 (1-46)
QY 1 ATGACAAAACCTTGAAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTCTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAAAACACCATCAAG 138
Db 41 LeuAlaAsnThrIleLys 46
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:38:26 ; Search time 88 Seconds
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Title: US-09-910-208B-12
Perfect score: 92
Sequence: 1 atgacaaaacttgaagagca.....attaccacaccacaagag 276

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1380268 seqs, 327241040 residues

Word size: 1

Total number of Hits satisfying chosen parameters: 2651796

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

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-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=oligo.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=500 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000
-USER=HADDAD-09-910208B @CGN 1 1 199 @runat_23022005_102318_15872 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	9	9.8	90	9	US-09-872-185B-11	Sequence 11, Appl
7	9	9.8	90	9	US-09-872-185B-12	Sequence 12, Appl
8	9	9.8	90	15	US-10-666-513-3	Sequence 3, Appli
9	9	9.8	90	16	US-10-665-867-3	Sequence 3, Appli
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; GENERAL INFORMATION:
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; TITLE OF INVENTION: Method for diagnosis of inflammatory diseases using Calgranulin C
; FILE REFERENCE: S30274US
; CURRENT APPLICATION NUMBER: US/10/077,600
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-077-600-2

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Score: 92.00 Matches: 92
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-910-208B-12 (1-276) x US-10-077-600-2 (1-92)

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; Sequence 41579, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2000-09-21
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QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276
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Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3
US-09-864-761-41579
; Sequence 41579, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

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; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41579
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011666.18
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.1
; OTHER INFORMATION: EST_HUMAN HIT: AV715719.1, EVALUE 1.00e-19
; OTHER INFORMATION: SWISSPROT HIT: P80511, EVALUE 1.00e-20
US-09-864-761-41579

Alignment Scores:
Pred. No.: 6.47e-37 Length: 46
Score: 46.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-864-761-41579 (1-46)

QY 1 ATGCAAAACTTGAAGAGCATCTGGAGGGAATGTCAATATCTTCACCAATACTCAGTT 60
|
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAGGGGCATTTTGACACCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
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Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTGCAACACCATCAAG 138
|
Db 41 LeuAlaAsnThrIleLys 46

RESULT 4
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-826-589-3 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
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Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 5
US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-4

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-826-589-4 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
|
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 6
US-09-872-185B-11
; Sequence 11, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-11

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-872-185B-11 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
|
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 7
US-09-872-185B-12

; Sequence 12, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-12

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9.78% Gaps: 0
DB: 9 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-872-185B-12 (1-90)

Qy 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 8
US-10-666-513-3
; Sequence 3, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAGE)
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Human
US-10-666-513-3

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9.78% Gaps: 0
DB: 15 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-666-513-3 (1-90)

Qy 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 9
US-10-665-867-3
; Sequence 3, Application US/10665867

; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-3

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9.78% Gaps: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-665-867-3 (1-90)

Qy 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 10
US-10-665-867-4
; Sequence 4, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-4

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9.78% Gaps: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-665-867-4 (1-90)

Qy 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 11
US-10-425-114-40894
; Sequence 40894, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 40894
LENGTH: 63
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(86)
OTHER INFORMATION: unsure at all Xaa locations
US-10-425-114-40894
Alignment Scores:
Pred. No.: 53.8 Length: 63
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 15 Gaps: 0
US-09-910-208B-12 (1-276) x US-10-425-114-40894 (1-63)
QY 134 TCAAGATATCAAGATAAAGCTG 157
Db 13 SerArgileSerLysIleLysLeu 20
RESULT 12
US-09-864-408A-6100
Sequence 6100, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Enco
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6100
LENGTH: 70
TYPE: PRT
ORGANISM: Homo sapiens
US-09-864-408A-6100
Alignment Scores:
Pred. No.: 52.9 Length: 70
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 11 Gaps: 0
US-09-910-208B-12 (1-276) x US-09-864-408A-6100 (1-70)
QY 167 TCATCAATGACAGCTTTATCTTG 144
Db 17 SerSerMetThrAlaLeuSerLeu 24
RESULT 13
US-10-424-599-151862
Sequence 151862, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 151862
LENGTH: 86
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(86)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_108155C.1.pap
US-10-424-599-151862
Alignment Scores:
Pred. No.: 51.2 Length: 86
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 15 Gaps: 0
US-09-910-208B-12 (1-276) x US-10-424-599-151862 (1-86)
QY 203 AGTCGACTTCAAGAAATTCATAT 226
Db 30 ArgSerThrPheLysAsnSerTyr 37
RESULT 14
US-10-363-829-311
Sequence 311, Application US/10363829
Publication No. US20040142331A1
GENERAL INFORMATION:
APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
APPLICANT: Gerstin, Jr., Edward H.; Panzer, Scott R.;
APPLICANT: David, Marie H.; Panzer, Scott R.;
APPLICANT: Flores, Vincent Z.; Daffo, Abel;
APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Inman, Rebekah R.
TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
FILE REFERENCE: PT-1183 USN
CURRENT APPLICATION NUMBER: US/10/363,829
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: PCT/US01/27628
PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/229,751
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,749
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,750
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,747
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,748
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/230,583

; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: LG:282729.1.orf1:2000SEP08
US-10-363-829-311

Alignment Scores:
Pred. No.: 44.6 Length: 206
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-363-829-311 (1-206)

Qy 79 ACCCTCTCTAAGGTGAGCTGAAG 102
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Db 31 ThrLeuSerLysGlyGluleuLys 38

RESULT 15

US-10-296-115-772
; Sequence 772, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 772
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-772

Alignment Scores:
Pred. No.: 44.2 Length: 218
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 15 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-296-115-772 (1-218)

Qy 79 ACCCTCTCTAAGGTGAGCTGAAG 102
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Db 31 ThrLeuSerLysGlyGluleuLys 38

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:27:10 ; Search time 29.5 Seconds
(without alignments)
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Ygapop 60.0 , Ygapext 60.0
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Delop 6.0 , Delext 7.0

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Word size: 1

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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	92	100.0	92	3	US-09-270-455-20
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4	9	9.8	51	3	US-09-270-455-2
5	9	9.8	90	4	US-09-263-312-3
6	9	9.8	90	4	US-09-826-589-3
7	9	9.8	90	4	US-09-826-589-4
8	9	9.8	91	3	US-08-794-000-2
9	9	9.8	91	4	US-09-646-651C-1
10	9	9.8	92	2	US-08-568-310D-19
11	9	9.8	92	3	US-09-270-455-19
12	8	8.7	103	2	US-08-585-585A-5

13	8	8.7	103	2	US-08-249-037C-5	Sequence 5, Appli
14	8	8.7	103	2	US-08-788-622B-5	Sequence 5, Appli
15	8	8.7	103	3	US-08-788-621B-5	Sequence 5, Appli
16	8	8.7	103	4	US-09-270-767-40569	Sequence 40569, A
17	8	8.7	103	4	US-09-270-767-55785	Sequence 55785, A
18	8	8.7	266	4	US-09-902-540-13043	Sequence 13043, A
19	7	7.6	62	4	US-09-328-352-7398	Sequence 7398, Ap
20	7	7.6	64	4	US-09-621-976-4767	Sequence 4767, Ap
21	7	7.7	90	4	US-09-904-615-141	Sequence 141, App
22	7	7.6	113	4	US-09-556-818-12	Sequence 12, Appl
23	7	7.6	114	4	US-09-540-236-3166	Sequence 3166, Ap
24	7	7.6	116	4	US-09-556-818-14	Sequence 14, Appl
25	7	7.6	116	4	US-09-556-818-52	Sequence 52, Appl
26	7	7.6	122	4	US-09-556-818-15	Sequence 15, Appl
27	7	7.6	122	4	US-09-556-818-16	Sequence 16, Appl
28	7	7.6	122	4	US-09-556-818-19	Sequence 19, Appl
29	7	7.6	122	4	US-09-556-818-48	Sequence 48, Appl
30	7	7.6	122	4	US-09-556-818-54	Sequence 54, Appl
31	7	7.6	124	4	US-09-556-818-13	Sequence 13, Appl
32	7	7.6	124	4	US-09-556-818-17	Sequence 17, Appl
33	7	7.6	124	4	US-09-556-818-46	Sequence 46, Appl
34	7	7.6	128	4	US-09-556-818-20	Sequence 20, Appl
35	7	7.6	128	4	US-09-556-818-50	Sequence 50, Appl
36	7	7.6	128	4	US-09-556-818-58	Sequence 58, Appl
37	7	7.6	130	4	US-09-556-818-18	Sequence 18, Appl
38	7	7.6	130	4	US-09-556-818-21	Sequence 21, Appl
39	7	7.6	130	4	US-09-556-818-56	Sequence 56, Appl
40	7	7.6	133	4	US-09-371-615A-8	Sequence 8, Appli
41	7	7.6	139	4	US-09-556-818-22	Sequence 22, Appl
42	7	7.6	145	4	US-09-556-818-60	Sequence 60, Appl
43	7	7.6	157	1	US-08-328-322-15	Sequence 15, Appl
44	7	7.6	160	4	US-09-107-532A-7069	Sequence 7069, Ap
45	7	7.7	171	4	US-09-134-000C-6448	Sequence 6448, Ap
46	7	7.6	174	1	US-08-328-322-17	Sequence 17, Appl
47	7	7.7	195	4	US-09-252-991A-28844	Sequence 28844, A
48	7	7.6	262	4	US-09-710-279-366	Sequence 366, App
49	7	7.6	264	4	US-09-107-433-2798	Sequence 2798, Ap
50	7	7.7	265	4	US-09-543-681A-6305	Sequence 6305, Ap
51	7	7.7	283	3	US-09-036-987A-13	Sequence 13, Appl
52	7	7.7	283	3	US-09-370-700-13	Sequence 13, Appl
53	7	7.7	283	4	US-09-603-207-13	Sequence 13, Appl
54	7	7.6	297	4	US-09-949-016-11547	Sequence 11547, A
55	7	7.7	305	4	US-09-599-360B-114	Sequence 114, App
56	7	7.6	310	4	US-09-902-540-13414	Sequence 13414, A
57	7	7.6	335	4	US-09-949-016-6262	Sequence 6262, Ap
58	7	7.6	345	4	US-09-252-991A-28350	Sequence 28350, A
59	7	7.6	359	3	US-09-134-001C-3728	Sequence 3728, Ap
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61	7	7.7	383	4	US-09-107-433-4404	Sequence 4404, Ap
62	7	7.7	442	2	US-08-821-355A-5	Sequence 5, Appli
63	7	7.7	442	2	US-09-003-687A-5	Sequence 5, Appli
64	7	7.7	442	3	US-09-136-605-5	Sequence 5, Appli
65	7	7.6	447	1	US-07-937-609-29	Sequence 29, Appl
66	7	7.6	447	1	US-07-978-892A-6	Sequence 6, Appli
67	7	7.6	447	3	US-08-029-170-29	Sequence 29, Appl
68	7	7.6	447	4	US-09-443-745-29	Sequence 29, Appl
69	7	7.6	448	1	US-08-570-157-3	Sequence 3, Appli
70	7	7.6	448	3	US-09-076-510-3	Sequence 3, Appli
71	7	7.6	448	4	US-09-004-349-3	Sequence 3, Appli
72	7	7.6	453	1	US-07-937-609-26	Sequence 26, Appl
73	7	7.6	453	1	US-07-937-609-27	Sequence 27, Appl
74	7	7.6	453	1	US-07-978-892A-5	Sequence 5, Appli
75	7	7.6	453	1	US-08-570-157-4	Sequence 4, Appli
76	7	7.6	453	3	US-08-029-170-26	Sequence 26, Appl
77	7	7.6	453	3	US-08-029-170-27	Sequence 27, Appl
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79	7	7.6	453	4	US-09-004-349-4	Sequence 4, Appli
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81	7	7.6	453	4	US-09-443-745-27	Sequence 27, Appl
82	7	7.6	458	4	US-09-693-746-6	Sequence 6, Appli
83	7	7.6	507	1	US-08-484-493-12	Sequence 12, Appl
84	7	7.6	507	1	US-08-484-494-12	Sequence 12, Appl
85	7	7.6	507	2	US-08-345-212-12	Sequence 12, Appl

86	7	7.6	507	3	US-09-249-003-12	Sequence 12, Appl	C 159	6	6.6	35	4	US-09-350-641C-234	Sequence 234, App
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C 118	6	6.6	35	3	US-09-082-279B-237	Sequence 237, App	C 191	6	6.6	51	4	US-09-513-999C-6538	Sequence 6538, Ap
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C 124	6	6.6	35	3	US-09-082-279B-243	Sequence 243, App	C 197	6	6.5	63	4	US-09-248-796A-25121	Sequence 25121, A
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C 128	6	6.6	35	3	US-09-315-304B-236	Sequence 236, App	C 201	6	6.5	67	4	US-09-270-767-55008	Sequence 55008, A
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C 130	6	6.6	35	3	US-09-315-304B-238	Sequence 238, App	C 203	6	6.6	72	4	US-09-252-991A-17145	Sequence 17145, A
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C 132	6	6.6	35	3	US-09-315-304B-240	Sequence 240, App	C 205	6	6.6	80	4	US-09-248-796A-23275	Sequence 23275, A
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ALIGNMENTS

RESULT 1
US-08-568-310D-20
; Sequence 20, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
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; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 20:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-20

Alignment Scores:
Pred. No.: 8.41e-84 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x US-08-568-310D-20 (1-92)

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RESULT 2
US-09-270-455-20
Sequence 20, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20

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STREET: 99 PARK AVENUE
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STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
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TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 20:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-09-270-455-20

Alignment Scores:
Pred. No.: 8.41e-84 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-270-455-20 (1-92)

QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCGAAACACCATCAAGAATATCAAGATAAAGCTGTCTATTGATGAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGTGAAGGCTGCCCATTAACACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3
US-08-568-310D-2
Sequence 2, Application US/08568310D
Patent No. 5976832

GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICANT NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 51
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 2:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 51
US-08-568-310D-2
Alignment Scores:
Pred. No.: 1.12 Length: 51
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-12' (1-276) x US-08-568-310D-2 (1-51)
QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20
RESULT 4
US-09-270-455-2
Sequence 2, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE

STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 51
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51
US-09-270-455-2
Alignment Scores:
Pred. No.: 1.12 Length: 51
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 3 Gaps: 0
US-09-910-208B-12 (1-276) x US-09-270-455-2 (1-51)
QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20
RESULT 5
US-09-263-312-3
Sequence 3, Application US/09263312
Patent No. 6555340
GENERAL INFORMATION:
APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: Extracellular No. 6555340el RAGE Binding Protein (EN-RAGE) and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 0575/55873-A
CURRENT APPLICATION NUMBER: US/09/263,312
CURRENT FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 90
TYPE: PRT
ORGANISM: Human
US-09-263-312-3
Alignment Scores:
Pred. No.: 1.05 Length: 90
Score: 9.00 Matches: 9

TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: ().()
OTHER INFORMATION: Angiotropin-related protein
US-09-646-651C-1

Alignment Scores:
Pred. No.: 1.05 Length: 91
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-646-651C-1 (1-91)

QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
|||||
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 10
US-08-568-310D-19
Sequence 19, Application US/08568310D
Patent No. 5976832
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92

US-08-568-310D-19

Alignment Scores:
Pred. No.: 1.05 Length: 92
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x US-08-568-310D-19 (1-92)

QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
|||||
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 11
US-09-270-455-19
Sequence 19, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92

Alignment Scores:
Pred. No.: 1.05 Length: 92
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-270-455-19 (1-92)

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; ADDRESS: Rae-Venter Law Gro

;
; ADDRESS: Rae-Venter Law Gro

;
; ADDRESS: Rae-Venter Law Gro

STREET: P.O.Box 60039
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,622B
FILING DATE: January 23, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,037
FILING DATE: 24-MAY-1994
APPLICATION NUMBER: US 07/865,095
FILING DATE: 08-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,987
FILING DATE: 25-OCT-1990
APPLICATION NUMBER: US 07/216,794
FILING DATE: 08-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Kung, Viola T.
REGISTRATION NUMBER: 41,131
REFERENCE/DOCKET NUMBER: CBDT.002.06US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-788-622B-5
Alignment Scores:
Pred. No.: 10.4 Length: 103
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-12 (1-276) x US-08-788-622B-5 (1-103)
QY 18 GCATCTGGAGGAATTGTCAATAT 41
Db 2 AlaSerGlyGlyAsnCysGlnTyr 9
RESULT 15
US-08-788-621B-5
Sequence 5, Application US/08788621B
Patent No. 6124117
GENERAL INFORMATION:
APPLICANT: Kilburn, Douglas G.
APPLICANT: Miller, Robert C.
APPLICANT: Warren, Richard A.J.
APPLICANT: Gilkes, Neil R.
TITLE OF INVENTION: Polysaccharide binding fusion proteins
TITLE OF INVENTION: and conjugates
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: P.O.Box 60039
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.

ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,621B
FILING DATE: January 23, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,037
FILING DATE: 24-MAY-1994
APPLICATION NUMBER: US 07/865,095
FILING DATE: 08-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,987
FILING DATE: 25-OCT-1990
APPLICATION NUMBER: US 07/216,794
FILING DATE: 08-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Kung, Viola T.
REGISTRATION NUMBER: 41,131
REFERENCE/DOCKET NUMBER: CBDT.002.05US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-788-621B-5
Alignment Scores:
Pred. No.: 10.4 Length: 103
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 3 Gaps: 0
US-09-910-208B-12 (1-276) x US-08-788-621B-5 (1-103)
QY 18 GCATCTGGAGGAATTGTCAATAT 41
Db 2 AlaSerGlyGlyAsnCysGlnTyr 9
Search completed: February 23, 2005, 12:40:09
Job time : 35.5 secs